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ALIGNMENTS

	CDS	source	FEATURES		JOURNAL	TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AX281582
<pre>/note="unnamed protein product" /codon_start=1</pre>	/organism="Homo sapiens" /db_xref="taxon:9606" 201489	11647	Location/Qualifiers	Arexis AB (SE)	Patent: WO 0177305-A 5 18-OCT-2001;	Variants of the human amp-activated protein kinase gamma 3 subunit	Anderson, L., Luthman, H. and Marklund, S.	1 (sites)	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens	human.		AX281582.1 GI:16608833	AX281582	5.	AX281582 1647 bp DNA linear PAT 02-NOV-2001	

BASE COUNT ORIGIN Query Match 100.0%; Best Local Similarity 100.0%; Matches 1647; Conservative (346 /protein_id="Cad10589.1"
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AJ249977.1 GI:6688200 AMP-activated protein

kinase;

AMPK

gamma

ω gene;

gamma

Homo sapiens human.

RESULT : HSA249977 LOCUS DEFINITION

Homo gapiens mRNA for AMP-activated (AMPK gamma 3 gene).

mRNA protein

kinase

PRI 07-APR-2000 gamma 3 subunit

REFERENCE AUTHORS

Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 2290)
Cheung, P.C., Salt, I.P., Davies

Davies, S.P., Hardie, D.G.

and Carling, D.

Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

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Direct Submission
Direct Submission
Submitted (12-OCT-1999) Carling D., Cellular Str
Clinical Sciences Centre, Hammersmith Hospital,
London, W12 ONN, UNITED KINGDOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Characterization of AMP-activated protein isoforms and their role in AMP binding blochem. J. 346 Pt 3, 659-669 (2000)
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KNRIHLLPVLDPYSGWYLHILTHKRLLKFLHIFGSLLPRFSFLYRTIQDIGIGTFRDL
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AUTHORS
TITLE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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VGLYSREDVIHLAAQOTYNHLDMSVGBALRQRTLCLEGVLSCQPHESLGEVIDRIARE
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 2 HSA249977 LOCUS DEFINITION

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HSA249977 Homo sapiens (AMPK gamma 3 AJ249977 ω mRNA gene) for 2290 bp 1 AMP-activated mRNA protein linear n kinase gamma

AJ249977.1 GI:6688200 AMP-activated protein human.

kinase;

AMPK

w

gene;

REFERENCE AUTHORS Chordata; Primates; Craniata; Vo Catarrhini; Vertebrata; i; Hominidae; Euteleostomi;

Homo sapiens
Eukaryota; Metazoa; C
Mammalia; Eutheria; P
1 (bases 1 to 2290)
Cheung, P.C., Salt, I.P .P., Davies ò . p . Hardie, ò and

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Direct Submission
Submitted (12-OCT-1999)
Clinical Sciences Centre
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LQCCFKPLVSISPNDSLFEAVYTLIKNRHHLPVLDPVSCHVLHILTHKRLLKFLHFF
GSILPRBSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVVNECGQV
VGLYSRFDVIHLAAQQTVNHLDMSVGEALRKTLCLEGVLSQQPHESLGEVIDRIARE
QVHRLVLVDETQHLGVVSLSDIQALVLSPAGIDPSGPEKI"
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/function="AMP-activated psubunit"
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1 Sciences Centre, Hammersmith Hospital, DuCane
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Andersson,L., Looft,C., Kalm,E., Milan,D., Robic, Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Chardon,P.
Variants of the gamma chain of ampk, dna sequence same, and uses thereof
Patent: WO 0120003-A 29 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (IN Andersson, Leif (SE); Looft, Christian (DE); Kundersson, Leif (SE); Looft, Christian (DE); Looft, Ch
                                                               9999t999cactccaccaacagggtgggactgcctcccctctgactgtacagcctcagct
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1 (bases 1 to 2115)

1 (bases 1 to 2115)

Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M., Rogel-Galliard,C., Paul,S., Tannuccelli,N., Rask,L., Ronne,H., Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.
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Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A.,
Rogel-Gaillard,C., Paul,S., Gellin,J., Lundstrom,K.,
Kalm,E., Le Roy,P., Chardon,P. and Andersson,L.
Direct Submission
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A mutation in PRKAG3 associated with excess glycogen
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/protein_id="AAF73987.1"
/db_xref="GI:8215682"
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/codon_start-1
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                                                                                                                                                                                                                                                                                                                                                 /gene="PKKAG3"
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                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="skeletal muscle"
1. .2115
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HLAAQQTYNHLDMSVGEALRQRTLCLEGVLSQPHESLGEVIDRIAREQVHRLVLVDDE
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Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                         same, and uses thereof
Patent: WO 0120003-A 31 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA)
Andersson, Leif (SE); Looft, Christian (DE); Kalm,
Location/Qualifiers
                                                                                                                                                                                           pig.
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalla; Eutheria; Cetartiodactyla; Suina; Suidae;
1 (bases 1 to 2022)
Andersson, L. Looft, C., Kalm, E., Milan, D., Robic, A.,
Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., le Roy
Chardon, P.
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/db_xref="taxon:9823"
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Science 288 (546
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Sus scrofa
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Milan, D., Jeon, J.T., Looft, C., Amarger, V., Robic, A., Rogel-Gaillard, C., Paul, S., Gellin, J., Lundstrom, K., Kalm, E., Le Roy, P., Chardon, P. and Andersson, L. Direct Submission
Submitted (10-DEC-1999) Dept Animal Breeding and General Computer (10-DEC-1999)
                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 1873)
Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M., Londstrom,K., Paul,S., Iannuccelli,N., Rask,L., Ronne,H., Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.
                                                                                                                                                                     Submitted (10-DEC-1999) Dept Animal Breeding University of Agricultural Sciences, BMC box
                                                                                                                                                                                                                                                                                               A mutation in
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ALVLSPAGIDALGA"
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Query Match
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Mammalia; Eutheria; Ct
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Sequence 27
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    Variants of the gamma chain of ampk, dna sequences ersame, and uses thereof
Patent: WO 012003-A 27 22-MAR-2001;
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Andersson, Leif (SE); Looft, Christian (DE); Kalm,
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                                                                     Andersson, L., Looft, C., Kalm, E., M. Rogel-Gaillard, C., Iannuccelli, N.,
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                                                                                            ; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Cetartiodactyla; Suina; Suidae;
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Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A., Rogel-Gaillard,C., Tannuccelli,N., Gellin,J. 12. Chardon,P.
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Andersson, Leif (SE); Looft, Christian (DE); Kalm,
Location/Qualifiers
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YRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVVNETGQVVGLYSRFDVI
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                      atccatcgcctgcctgttcttgacccggtgtcaggcaacgtactccacatcctcacacac
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Characterization of AMP-activated protein kinase subunits. Assembly of the heterotrimeric complex J. Biol. Chem. 271 (17), 10282-10290 (1996)
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FVQHRVSALPVVDEKGRVVDIYSKFDVINLAAEKTYNNLDVSVTKALQHRSHYEGVL
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U42413.1
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Direct Submission
Submitted (07-DEC-1995) Le
Dartmouth Medical School,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 155)
Gao, G., Widmer, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gao,G., Fernandez,C.S., Stapleton,D., Auster,A.S., Dyck,J.R., Kemp,B.E. and Witters,L.A.
Non-catalytic beta- and gamma-subunit isoforms of the state of the state
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Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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/protein_id="AAC52580.1"
/db_xref="GI:1335860"
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EHKIETWREVYLQDSFKPLVCISPNASLFDAVSSLIRNKIHRLPVIDPESGRYLYILT
HKRILKETKLETTEFFKPEFMSKSLEELGIGTFYANIAWYRTTTDYVALGIFVOHRVS
ALPVVDEKGRVVDIYSKEDVINLAAEKTYNNLDVSVTKALGHSSHYFEGVLKCYLHET
LEAIINRLVEAEVHRLVVVDEHDVVKGIVSLSDILQALVLTTGGEKKP*
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/db_xref="taxon:10116"
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/product="5'-AMP-activated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (07-DEC-1995) Lee A. Witters, Medicine/Biochemistry, Medical School, N. College St., Hanover, NH 03755-38
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AAGGGCATTGTATCGCTGTCTGACATCTTACAGGCTCTGGTGCTCA
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                                                     TCACACTACTTCGAGGGTGTTCTCAAGTGCTACCTACATGAGACTCTAGAAGCAATCATC
                                                                                                   acactatgtctggagggagtcctttcctgccagccccacgagagcttggggggaagtgatc
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                                                                                                                                  GCAGCAGAAAAGACATACAACCAACCTAGATGTGTGTGACAAAAGCCCCTACAGCACCGG
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Ax281579
Ax281579.1
                                                                                                                                                                                           196554 bp DNA
Homo sapiens chromosome 2 clone RP11-64705,
17 unordered pieces.
AC073128
         The sequence of Homo sapiens clone 
Unpublished
                                                                     Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                         AC073128.3 GI:13027579
HTG; HTGS_PHASE1; HTGS_DRAFT;
                                               Waterston, R.H.
                                                                                                                      Homo sapiens
                                                                                                                                          human.
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/db_xref="taxon:9606"
306 c 286 g 16
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from Patent WO0177305
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99.38;
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Pred. No. 1.3e-82;
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                                                                              Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                     HTGS_FULLTOP
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Catarrhini; Hominidae,
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DRAFT SEQUENCE,
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TITLE
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                                                         FEATURES
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                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing vector: M13; 98%
Sequencing vector: plasmid; 0%
Sequencing vector: plasmid; 0% of reads
Chemistry: Dye-primer ET; 98% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 187795 bases at least Q40
Consensus quality: 190513 bases at least Q30
Consensus quality: 192099 bases at least Q20
Insert size: 200000; agarose-fp
Insert size: 194954; sum-of-contigs
Quality coverage: 5.58 in Q20 bases; sum-of-contigs
Quality coverage: 5.57 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (08-JUN-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Feb 21, 2001 this sequence version replaced g1:8469048.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center project name: H_NH0647005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: Washington University Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                        28888
28988
35356
44643
44743
44743
58276
58276
73817
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11857
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1258
3601
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                                                   Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                     .196554
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                                                                                                                                               8624: gap of 11956: gap of 15783: contig 15783: contig 15883: gap of 21906: contig 28987: gap of 28987: gap of 35255: contig 35255: contig 35275: gap of 44642: contig 35275: contig 58275: contig 582
                                                                      130425: gap of unknown length
149287: contig of 18862 bp in
149387: gap of unknown length
196554: contig of 47167 bp in
                                                                                                            130425: gap of
149287: contig
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of 3321
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g of 1403
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of 6881
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of 3232
                                                                                                                                             of 16888 bp in
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of 18224 bp in
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                                                                      gcctgccctgtgcctgtccccgcaggccccatttcccaagctgggctgggatgacgaact
                                                                                                                       CACCGAGTTCCCAGCCACAGAGGCCTGGGGAGTGTGAGCTAGAAGGCCTGCTGGAAGAGAG
                                                                                                                                   cacggagttcccagccacagaggcctgggagtgtgagctagaaggcctgctggaagagag
catggcaactagctccaagctagtcatcttcgacaccatgctggagatcaag
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130426 . 149287
/note="assembly_name:Contig32"
149388 . .196554
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46993 c 45889 g
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clone_end:SP6
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92241. .113337
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73917. .92140
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44743. .58275
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22007. .28887
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15884. .21906
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8625. .11856
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5204. .8524
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1258. .
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28988. .35255
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/note="assembly_name:Contig19
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/clone="RP11-64705"
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Pred. No. 7.8e-83;
0; Mismatches 3
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Shamsadin, R., Jantsan, K., Adham, I. and Engel, W. Cloning, organisation, chromosomal localization analysis of the mouse Prkagl gene Cytogenet. Cell Genet. 92 (1-2), 134-138 (2001) 21203559
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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/product="AMP activated protein kinase"
/protein_id="AAB95475.1"
/protein_id="AAB95475.1"
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WTLYILTHKRILKFLKLFIIEFPKPEFWSKSLQELQIGTYANLAWATTTPVVVVALGI
FVQHRYSALPVVDEKKRVLVFIIEFPKPEFWSKSLQELQIGTYANLAWATTTPVVVALGI
FVQHRYSALPVVDEKKRVLVFVDEHXXVKGIVSLSDILQDLVLTGGEKKP"
ACYLHETLETIINRLUEEBVHRLVVVDEHXXVKGIVSLSDILQDLVLTGGEKKP"

414 c 416 g 400 t 10 others
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Email: cgapbs r@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human

center, Stanford University School of Medicine, Stanford,

center, Stanford.edu

Contact: (Dickson, Mark) mcd@paxil.stanford.edu

Contact: (Dickson, Mark) mcd@paxil.stanford.edu

Contact: (Dickson, Mark) mcd@paxil.stanford.edu
                                                                                                                                                                                             Direct Submission
Direct Submission
Submitted (01-OCT-2001) National Institutes of Health, Mammalian Submitted (01-OCT-2001) Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Traffitute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 3132)
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Contact: MGC help desk
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TCATGAAGCAGAACCTGGATGAGCTTGGAATCGGAACGTACCACAATATTGCCTTCATTC
                                 tcctctaccgcactatccaagatttgggcatcggcacattccgagacttggctgtggtgc 1106
                                                                       ATAAAATCCACAGATTGCCAGTTATTGACCCTATCAGTGGGAACGCACTTTATATACTTA
                                                                                                                                                                  accggatccatcgcctgcctgttcttgacccggtgtcaggcaacgtactccacatcctca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov series: IRAK Plate: 25 Row: i Column: 18
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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MPLLDGDVENSEKHSSRKUDSPFSSGSPSRGLFSRGPQPFPSSPVSAFVRFKTSPGSP
KTVFFPSVQESPFRSPKRMSFGGIFRSSSKESSPNSNPSTSPGGIFFFSSKKTSSVS
SSPSTPTQVTKQHFFPLLSYKQBFERFSSIYASSSPDTTGQRFCLAFQSPARPPLAS
SSPSTPTQTTKQHFFPLLSYKQBFERPSSIYASSSPDTTGQRFCLAFQSPARPPLAS
SPYHAPLRTAVLAAAPGPAEAGMLEKLEFQEEEDSESGFYMRFMRSHKCYDIVPTSSK
LVVFDTTLQVKKAFFALVANGVAAAPLMESKKQSFVGMLTITDFINILHRYYKSPMVQ
IYELEEHKIETTWRELYLQETFKPLWISPDASLFDAVYSLIKHKIHRLPVIDPISGNA
LYILTHKRILKFLQLFMSDMPKPAFMKQNLDELGIGTYHNIAFIHPDTPIIKALNIFV
ERRISALFVVDESGKVVDIYSKFDVINLAAEKTYNNLDITVTQALQHBSQYFEGVVKC
SKLETLETIVDRIVRAEVHRLVVVNEADSIVGIISLSDILQALILTPAGAKQKETETE
KLETLETIVDRIVRAEVHRLVVVNEADSIVGIISLSDILQALILTPAGAKQKETETE
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/db_xref="taxon:10990"
/clone="MGC:18882 IMAGE:4238045"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="Unknown (protein /protein_id="AAH15283.1" /db_xref="GI:15929720"
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/clone_lib="NCI_CGAP_Kid14"
/lab_host="DH10B"
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Scarch completed: October 3, 2002, 14:48:55 Job Lime: 12055 sec

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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BJ0772114 BM48865 zpmZn.pk0
BM487789 pgmZn.pk0
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BM440762 pgrIn.pk0
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AJ395115 AJ395115
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AV603335 AV603357
B1833269 603087149
AA558845 n169b09.s
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AA578219 n156h03.s
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AL555228 AL552459 AL548987	AL519198 BI546514 BI858240 BI910928 BG177822	B1819312 B1821538 BE871189 B1771184	BG705895 AW411228 BI223706 BI768590 BI914634 BF528081 B1859947	BG09812 AW410926 BE148626 AW956906 BG740148	AL047390 BE166881 BE166874 AW379936
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ALIGNMENTS

VERSION KEYWORDS SOURCE ORGANISM RESULT 1 BI344527 LOCUS DEFINITION FEATURES COMMENT REFERENCE ACCESSION JOURNAL TITLE AUTHORS source BI344527 373008 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence. BI344527 BI344527.1 GI:15037807 EST. pig. Sus scrofa Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4366
Email: smithemail.marc.usda.gov
Email: smithemail.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. vector identified by cross_match with the -minscore 18
and minmatch 12 options. PCR PRIMERS
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine Unpublished (2000) Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. Plate: 119 row: I column: 11 Seq primer: ATTTAGGTGACACTATAG. and Keele, J.W. (bases 1 to 572) /organism="Sus scrofa" /db_xref="taxon:9823" /clone_lib="MARC 2PIG" /tissue_type="pooled" /note="Vector: /lab_host="DH10B" Location/Qualifiers pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; EST 30-JUL-2001

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BASE COUNT
ORIGIN
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ORGANISM
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Fax:
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                              Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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zp38d10.r1 Stratagene muscle 37209 Homo sapiens cDNA clone
IMAGE:611731 5' similar to SW:AAKC_RAT P80385 5'-AMP-ACTIVATED
PROTEIN KINASE, GAMMA CHAIN ;, mRNA sequence.
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     /dev_stage="adult"
/lab_host="Solte" (Kanamycin resistant)"
/lab_host="Solte" (Kanamycin resistant)"
/note="organ: skeletal muscle; Vector: pBluescript SK.
/note="organ: skeletal muscle; Cloned unidirectionally.
Site_1: EcoRI; Site_2: xhoI; Cloned unidirectionally.
Primer: Oligo dT. Skeletal muscle from patient with
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                                                                                                                                                         /clone_lib-"Stratagene muscle 937209"
/tissue_type="muscle"
                                                                                                                                                                                              /clone="IMAGE:611731"
                                                                                                                                                                                                              /db_xref="taxon:9606"
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                                                                                                                                                                                                                              /db_xref="GDB:4643570"
                                                                                                                                                                                                                                                ∕organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                      Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part o scale clone-end sequencing project of the Tetraodon nigrov genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
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Roest-Crollius, H., Ja
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GSS; genome survey sequence.
Tetraodon nigroviridis.
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/note="Genoscope sequence ID : C0BG033CF07LP1-end : T7"
/note="Genoscope sequence ID : C0BG033CF07LP1-end : T7"
/ 282 c 241 g 271 t 6 others
                                                                                                                                                                                                                         /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
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,C., Wincker,P., Brottier,P., Quetier,F.,
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0; Mismatches 3
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                  found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM10895 row: d column: 22
                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sa
Site_2: NotI; Cloned unidirectionally. Primer: Oligo of
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"
a 292 c 238 g 159 t
                                                                   /db_xref="taxon:10090"
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                 Unpublished (2001)
Contact: Tadasu Sh
                                                                                                                                                                                                            National Institute of Genetics
1111 Yata, Mishima, Shizuoka 4
                                                                                                                                                                                                                                              Center For Genetic Resource Information
                                                                                                                                                                                                                                                                                                                                               Kitayama,A.,
                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; (Amphibia; Batrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BJ072114
BJ072114.1 GI:17502303
EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BJ072114 HIBB Mochii normalized Xenopus tailbud laevis cDNA clone XL096j16 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                       Expressed genes in X. laevis embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                             African clawed frog.
                                                                                                                                                                                                                                                                                                                                                                                       (enopodinae;
                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to
                                                                                                                                                                          1 Yata, Mishima,
: 81-559-81-6856
: 81-559-81-6855
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                                                                                                                                                      tshini@genes.nig.ac
                                                        /organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="XL096j16"
                                                                                                                        Location/Qualifiers
                                    /clone_lib="NIBB Mochii normalized
′tissue_type≈"whole embryo"
                                                                                                                                                                                                                                                                                                                                                                                                 Metazoa; Chordata; Craniata; Vej
Batrachia; Anura; Mesobatrachia;
                                                                                                                                                                                                                                                                                                                                                                                   Xenopus.
                                                                                                                                                                                                                                                                                                                                           Terasaka,C.,
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                                                                                                                                                                                                                                                                       Shin-i
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Pred. No. 7.2e-08;
                                                                                                                                                                                                                                                                                                                                           Mochii, M.,
                                                                                                                                                                                                        411-8540, Japan
                                                                                                                                                                                                                                                                                                                                           Ueno, N.,
                                                                                                                                                                                                                                                                                                                                                                                                   Vertebrata;
ia; Pipoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                      Xenopus tailbud
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                                                                                                                                                                                                                                                                                                                                           Shin-i,T. and Kohara
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Pipidae;
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1 (bases 1 to 536)
Cogburn, L. A. and Monsonego-Ornan, E.
Cogburn, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cogburn@udel.edu, www.chickest.udel.edu.
Location/Qualifiers
                                                                      /note="Vector: pCMVSPORT6; Library made from equivalent pools of total RNA isolated from each tissue (embryonic muscle 33.3%; juvenile muscle 33.3%; and epiphyseal growth plate 33.3% of the final RNA pool). Single pass sequencing from 5'-end"
                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="Breast muscle, leg muscle and
growth plate"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /Clone="pgm2n.pk008.g21"
/clone_lib="Normalized Chicken Breast Muscle, Leg
and Epiphyseal Growth Plate cDNA library (pgm2n)"
/sex="Male and Female"
                                                                                                                                                                                                                                                                                                    /dev_stage="Breast,leg:Embryo(dl9);post-hatch(ld,1,3,5,7,9,11 weeks);growth plate(ld,7d,14d post-hatch)"
/lab_host="E. coli EMDH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="Commercial broiler and Strains 90 & 21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9031"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Gallus gallus"
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Pred. No. 7
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                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Larry A. Cogburn University of Delaware Townsend Hall, Newark, DE 1 Tel: 302-831-1335
Fax: 302-831-2822
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Cogburn, L.A. and Monsonego-Ornan, E.
ESTs from Normalized Chicken Breast Muscle, Leg Muscle,
Epiphyseal Growth Plate cDNA library, USDA/IFAFS Animal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
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                                                                                                                                                                                                                                                                                                                                                                          cogburn@udel.edu, www
Location/Qualifiers
               ø
       /dev_stage="Breast,leg:Embryo(d19):post-hatch(ld,1,3,5,7,9,1 weeks):growth plate(ld,7d,14d post-hatch)"
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199 c 137 g 133 t
                                                                                                                                                                                                             /tissue_type="Breast muscle,
growth plate"
                                                                                                                                                                                                           and Epiphyseal Growth Plate /sex="Male and Female"
                                                                                                                                                                                                                                                                                                     /strain="Commercial broiler
Strains 90 & 21"
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Pred. No. 8.4e-08
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Score 80.2; DB Pred. No. 2e-07; 0; Mismatches

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                                                                                    CCTCCCCGTCATCGACCCCGACTCGGGCAACACTCTCTACATCCTCACCCACAAACGCAT
                                                                                                                         CTCCCCCAATGCCAGCCTTTTTGATGCCGTCTCCTCCCTGATCCGCAATAAGATCCACCG
                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2001)
Contact: Joan Burnside
Molecular Endocrinology
University of Delaware
40 Townsend Hall, Newark, DE 19717, U:
Tel: 302 831-1345
Fax: 302-831-3411
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BG7116. pk008.c13 Normalized Liver Library Gallus gallus cDNA clone pglln. pk008.c13 S similar to gi[4506061 ref[NP_002724.1] protein kinase, AMP-activated, gamma 1 non-catalytic subunit; AMPK gamma 1; Protein kinase, AMP-activated, noncatalytic, gemma-1 [Homo sapiens] gi[127373489 ref[XP_006778.2] protein kinase, AMP-activated, gamma 1
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                                                                                                                                                                                                                                                            /tissue_type="liver"
/lab_host="E.coli EMDH10B"
/note="Vector: pCMVSPORT 6'
215 c 167 g 119 i
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/clone="pg11n.pk008.c13"
/clone_lib="Normalized Liver
/sex="Male and Female"
                                                                                                                                                                                                                                                                                                                                                                      organism="Gallus gallus"
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Byrln.pk002.19 Normalized Chicken Reproductive Tract cDNA Library (pgrln.pk002.19 Sommalized Chicken Reproductive Tract cDNA Library (pgrln) Gallus gallus cDNA clone pgrln.pk002.19 5' similar to gl14506061 ref|NP_002724.1| protein kinase, AMP-activated, gamma 1 non-catalytic subunit; AMPK gamma 1; Protein kinase, AMP-activated, noncatalytic, gemma-1 [Homo sapiens] gi|12737489 ref|XP_006778.2| protein kinase, AMP-activated, gamma 1, mRNA sequence.
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chicken.
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Townsend Hall, Newark, DE 19717,
Tel: 302-831-1335
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Contact: Larry A.
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ESTs from Normalized Chicken Reproductive Tract cDNA library-
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nilarity 69.4%;
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Location/Qualifiers
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/dev_stage="Various stages;embryonic, post-hatch, immature
and sexually-mature"
/lab_host="E. coli_EMDH10B"
/note="Vector: pCMVSPORT6; Library made from three total
RNA pools from each tissue (testis 25%, ovary 25%, and
oviduct 50% of final RNA pool); Single pass sequencing
from 5'-end"
a 222 c 160 g 128 t
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/strain="Commercial broiler
/db_xref="taxon:9031"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Library (pgrln)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="pgrln.pk002.19"
/clone_lib="Normalized Chicken Reproductive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 80.2; DB 10;
Pred. No. 2.1e-07;
0; Mismatches 48;
                                                                  649 bp
gallus c
                                                                    cDNA clone 21c2r1,
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                                                                                          mRNA
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SOURCE
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Best Local :
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                             source
                                                                                                    chicken.
ISM Gallus gallus
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
Archosauria; Aves: Neognathae: Galliformes; Phasianidae;
Phasianinae: Gallus.

NCE 1 (bases 1 to 758)
ORS AbdrakhmanovI. Lodygin,D., Geroth,P., Arakawa,H., Law,A., Plachy
J., Korn,B. and Buerstedde,J.M.
A large database of chicken bursal ESTs as a resource for the
analysis of vertebrate gene function
Genome Res. 10 (12), 2062-2069 (2000)
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AJ396118 dki
AJ396118
AJ396118.1
                                  Cellular Immunology
Heinrich-Pette-Institute
Heinrich-Pette-Institute
Martinistr. 52, 20251 Hamburg, Germany
Martinistr. 51, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
                                                                                                                                                                                                                                                                                                            EST
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A large database of chicken bursal ESTs as a resource for the Genome Res. 10 (12), 2062-2069 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Heinrich-Pette-Institute
Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
Location/Qualifiers
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Gallus gallus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Buerstedde JM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Gallus gallus"
/strain="CB"
/db_xrefe="taxon:9031"
/clone="21c2r1"
/clone_lib="dkfz426"
                                                                                                                                                                                                                                                                                                                                                     dkfz426 Gallus
          /organism="Gallus gallus"
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227 c 155 g 137 t
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Pred. No. 2.1e
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                                                                                                                                                                                                                                                                                                                                               Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fuku
Tel: 81-248-25-5641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AV603335
AV603335
5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic Acids Res. 29 (22), E108 (2001) 21570554
                                                                                                                                                                                                                                                                                                Single pass sequencing.
                                                                                                                                                                                                                                                                                                            Email: kazusugi@cocoa.ocn.ne.jp
                                                                                                                                                                                                                                                                                                                                   Fax: 81-248-25-5725
                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Yoshikazu Sugimoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Establishment of a high throughput EST sequencing system using poly(A) tail-removed cDNA libraries and determination of 36,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and Sugimoto, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Takasuga, A.,
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EST.
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AV603335
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                                                                                  144
                                                                                                                                                                                                                                                                       clone was obtained from a polyA-deleted cDNA library.
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                                                                                                                           /organism."Bos taurus"
/db_xref="taxon:9913"
/clone="ERK1015P02"
/clone_lib="Bos taurus kidney fetus"
/tissue_type="kidney"
/dev_stage="fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="CB"
/db_xref="taxon:9031"
/clone="25f16f1"
/clone_lib="dkf2426"
/tissue_type="Bursa of Fabricius"
a 238 c 186 g 166 t
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                                                                           /note="Vector: p2L1; Site_1:
was deleted from a Not1 site"
150 c 122 g 158 t
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 4.48;
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Score
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76.4; DB 9;
No. 1.4e-06;
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                                                                                                            Sall; Site_2:
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             Length 576;
                                                                            2 others
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                                                                                                                                  94; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Yoshikazu Sugimoto
Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fuku
Tel: 81-248-25-5641
                                                                                                                                                                                                                                                                                                                                                                        This clone was obtained from a polyA-deleted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Establishment of a high throughput EST sequencing system using poly(A) tail-removed cDNA libraries and determination of 36,000 bovine ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5', mRNA sequence, AV608257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AV608257

564 bp mRNA linear EST 28-NOV-2001 AV608257 Bos taurus kidney fetus Bos taurus cDNA clone E1K1045H03 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                        Single pass sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: 81-248-25-5725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and Sugimoto, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST.
                                                                                                                                                                                                                                                                                                                                                                                                     Email: kazusugi@cocoa.ocn.ne.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21570554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus
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                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                 /organism="Bos taurus"
/db_xref="taxon:9913"
/clone="ElK1045H03"
/clone_lib="Bos taurus kidney fetus"
/tissue_type="kidney"
/dev_stage="fetus"
                                                                                                                                                                                                           /note="Vector: pZL1; Site_1: Sal1; Site_2: was deleted from a Not1 site" 145 c 121 g 155 t 1 others
                                                                                                                                                                                                                                                      /lab_host-"DH10B"
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                                                                                                                                             4.28;
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                                                                                                                             Score 73; DB 9; Le
Pred. No. 7.7e-06;
0; Mismatches 36;
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RESULT 15
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                                                                                                                                                                                                                               TGACCCAGAATCAGGCAATACTTTGTACATCCTCACCCACAAGCGCATTCTGAAGTTCCT
AA558845
448 bp mRNA linear EST 09-SEP-1997 nl69b09.sl NCI_CGAP_Pr4.l Homo sapiens cDNA clone IMAGE:1045913 similar to SW:AAKG_RAT P80385 5'-AMP-ACTIVATED PROTEIN KINASE,
                                                                                                                                                                                                                                                                                                                                                                                               98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAMI1569 row: a column: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 775)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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Clone distribution: MGC clone distribution information can
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PONTE "Organ: pooled pancreas and spleen; Vector: pcMV-SPORT6; Site_1: NotI; Site_2: ECRV (destroyed): RNA source anonymous pool of spleen and pancreas from 28 yo male. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 0.25. Note: this is a NHH_MGC Library." a 194 c 171 g 209 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:5226132"
/clone_lib="NIH_MGC_120"
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/db_xref="taxon:9606"
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68.18;
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Pred. No. 2.5e-05;
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Best Local Similarity 68.18;
Matches 98; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unupublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 561 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 297.
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NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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AA558845
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//lab_host-"DH10B"

//note-*Organ: prostate; Vector: pAMP10; mRNA made from prostatic intrapplithelial neoplasia (high-grade), cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. cDNA Library Preparation: David B. Krizman, Ph.D. Reference: Krizman et al. (1996) Cancer Research ph.D. 56:5380-5383. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center.
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/db_xref-"taxon:9606"
/clone="IMAGE:1045913"
/clone_llb-"NCI_CGAP_Pr4.1"
/sex-"male"
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grade"
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Pred. No. 2.6e-05;
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Maximum Match 100%
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Perfect score:
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Copyright (c) 1993 - 2000 Compugen Ltd
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ALIGNMENTS

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                             Sequence 3 from Patent WO0177305. AX381580
                                                                                    Andersson, L., Luthman, H. and Marklund, S. Variants of the human amp-activated protein kinase gamma 3 subunit Patent: WO 0177305-A 3 18-OCT-2001; Arexis AB (SE)
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AUTHORS TITLE JOURNAL REFERENCE AUTHORS ACCESSION VERSION KEYWORDS SOURCE RESULT 2 AC027416/c LOCUS REFERENCE DEFINITION ORGANISM Unpublished

2 (bases 1 to 152129)

2 (bases 1, Linton, L., Nusbaum, C., Lander, E., Abraham, H., A Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., A Anderson, S., Baldwin, J., Barna, N., Bastlen, V., Bedd, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campoplano, A., Castle, A., Cheepel, Y., Colangelo, M., Collin Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhigh, W., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., unordered pieces.
AC027416
AC027416.2 GI:8317289
HTG; HTGS_PHASE1; HTGS_DRAFT. Birren, B., Linton, L., Nusbaum, C. Homo sapiens, clone RP11-504G11 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 152129) AC027416 Homo sapiens Homo sapiens clone 152129 I RP11-504G1 <u>,</u> pp DNA and Lander, linear HTG DRAFT SEQUENCE, Hominidae; Collins, S Euteleostomí; 07-JUN-2000 32 Gage, D., Allen, N.,

COMMENT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (30-MAR-2000) whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 7, 2000 this sequence version replaced gi:7342115. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 135376 bases at least Q40 Consensus quality: 135264 bases at least Q30 Consensus quality: 146503 bases at least Q20 Insert size: 161000; agarose-fp Insert size: 149029; sum-of-contis Quality coverage: 3.1 in Q20 bases; sum-of-contigs Quality coverage: 3.3 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Young,G., Zainoun,J., Zimmer,A. and Zody,M.
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Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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996 66695: gap of 100 bp
996 73218: contig of 6523 bp in length
1997 73318: gap of 100 bp
177115: contig of 3797 bp in length
16 77215: gap of 100 bp
16 77215: gap of 100 bp
17 85022: contig of 7807 bp in length
18 5122: gap of 100 bp
18 93314: contig of 8192 bp in length
19 93414: gap of 100 bp
19 93414: gap of 100 bp
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11 10193: contig of 7779 bp in length
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123496: contig of 10306 bp
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152129: cont
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419: gap of 100 bp
27059: contig of 2640 bp in length
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Best Local Similarity 99.9%;
Matches 1720; Conservative
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                                        actytcctyttcccacaytccccactytytctcaycacaayyacactyycayyytyyya
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                                                                                                                                                                  9939tct9cat999cca9ct999agaccct9999ctcaatttccccatctgt9gagccgct
                                                                                  AGCAAATGGGGGGAGGCAGGAGAAAGAGCCCCCACTTCTCAGGCCTGGGGGGCTGCCCC
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60996. .66595
/note="assembly_fragment"
66696. .73218
/note="assembly_fragment"
77319. .77115
/note="assembly_fragment"
77216. .85022
/note="assembly_fragment"
85123. .93314
/note="assembly_fragment"
93415. .101193
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101294. .113090
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51386. .55871
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46466. .51285
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42467. .46365
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38280. .42366
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/note="assembly_fragment"
27160. .30170
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34069...38179
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Pred. No. 0;
0; Mismatches
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1680	l catcctgactgcactggacatctttgtggaccggcgtgtgtctgcactgcctgtggtcaa	1621	Qy
9		35058	Db
1620	. tatccaagatttgggcatcggcacattccgagacttggctgtggtgctggagacagcac	1561	Qy
1560 35059	1 acctggtccccatcctaaccagggttccctgctgccccggccctccttcct	150 3511	Db 04
1500 35119	1 ccctagcagtcgtggggaagagctgggagccctcttgaagctgctggatccctgatctcc 	17	Дy
1440 35179	1 cccaggtgggaggaaggggagacctgggcaggtgatcagagggcctgaggagtcttcag 	23	Дb
1380 35239	1 actecacatecteacacacaaacgeetgeteaagtteetgeacatetttgtaageetggg	29	Qy
1320 35299	1 caccotcatcaagaaccggatccatcgcctgcctgttcttgacccggtgtcaggcaacgt	35	Оy
1260 35359	1 ctccctaggctgccccgaggctcactgctcccatctctgcagcctgtttgaagctgtcta 	20	Оу
1200 35419	1 cagacaagggagccttggtgccctgccctccttttaggggcctgggatggaggttgtct 	114 3547	Оу
1140 35479	1 acagicoceticoccagicocacicagetetgaacteaceteticatectaggeggeaca 	53	Qy Db
1080 35539	1 ctccatctctcctaatgataggtgggtgtctcttgctcatcacctgagcctcctcctccccllllllllll	102 3559	Оy
1020 35599	1 tggcctgactctggctctttctgcagagatctacctgcaaggctgcttcaaggcctctggt 	3565 3565	Ор
960 356 5 9	1 99tgcctgacggaagggaagctgcctgggactgcaaggtgaaggcaggtgaccggctcccc 	90 3571	Оу
900 35719	1 gtggaggatgggcagtggggatgtcctggagtgaacaggggaggga	84 3577	ОУ
840 35779	1 999t9a9t9999a9a99aaccc99aaa9999ct9tt9gt9at99t9g9cca999cttaa9 	78 3583	Оу
780 35839	1 ctgtcgatgtctctaggtccagatctatgagattgaacaacataagattgagacctggag 	72 3589	Qy
720 35899	1 aggggagtcctcctggagcctggtgccctagaagcccacgtctttctgacttctggagtc 	3595	Db Oy
660 35959	1 ggtccccctggtgaggagtgggctgggaatcttatgggcacccagaggggcggggll	60 3601	ОУ
600 36019	ctcccctgcagggatgctgaccatcactgacttcatcctggtgctgcatcgctactaca	54 3607	Qy Db

VERSION KEYWORDS SOURCE

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REFERENCE

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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing vector: M13; 988
Sequencing vector: M13; 988
Sequencing vector: plasmid; 08
Chemistry: Dye-primer ET; 988 of reads
Chemistry: Dye-terminator Big Dye; 08 of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 187795 bases at least Q40
Consensus quality: 190513 bases at least Q30
Consensus quality: 192099 bases at least Q20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission

Sequencing Center, Washington Submitted (08-JUN-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center project name: H_NH0647005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Washington University Genome Sequencing Center Center code: WUGSC
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Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Insert size: 200000; agarose-fp
Insert size: 194954; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence of Homo sapiens clone
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                                                                                                                                                                                                                                                                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                             as soon as it is available and the accession number will be preserved.
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                                   1157: contig of 1257: gap of 0 3600: contig of 3700: gap of 0 5203: contig of 25203: contig of 8524: gap of 11856: contig of 11856: contig of 15783: contig of 15883: gap of 15783: contig of 15883: gap of 15883: g
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unknown
of 3232
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of 2343
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unknown length
                    O.f.
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Best Local Similarity
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/db_xref="taxon:9606"
/chromosome="2"
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73816: contig of 15441 bp in 16
73916: gap of unknown length
73916: gap of unknown length
92140: contig of 18224 bp in 16
92240: gap of unknown length
113337: contig of 21097 bp in 16
113437: gap of unknown length
130325: contig of 16888 bp in 16
130425: gap of unknown length
149287: contig of 18862 bp in 16
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 206854)
Sulston,J.E. and Waterston,R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
99067792
4 (bases 1 to 206854)
Waterston,R.H.
Direct Submission
Submitted (08-NOV-2001)
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                                              Submitted (08-SEP-1999) Genome University School of Medicine, MO 63108, USA
                                                                                 Waterston, R.H.
Direct Submission
                                                                                                          The sequence of Homo sapiens Unpublished (2001)
3 (bases 1 to 206854)
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Submitted (09-JAN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 6
On Nov 8, 2001 this sequence version replaced gi:13431203.

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Genome Sequencing Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission Submitted (03-JAN-2002) Genome Sequencing Center, Washington
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                                                                                                                                                                                                                                                                                                                             The clone sequenced to the left is RP11-1077K22; the clone sequenced to the right is RP11-64705. Actual start of this clone is at base position 1 of RP11-459119; actual end is at base position 206854 of RP11-459119.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. 1 MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                         Data from AC079810 and AC073128 was used to finish this clone, AC009974. Polymorphisms have been identified between AC073128 AC009974. A single plasmid region exists betten 38812-38903 unresolved tandem in the HERV SVA exists between 184390-185163.
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                                                                                                                                                                                                                                                                                                                                                                                                           VECTOR: pBACe3.6
NEIGHBORING SEQUENCE INFORMATION:
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Contact: sapiens@watson.wustl.edu
------ Summary Statistics
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  /note="match to EST BE314060 (NID:g9134719)"
                                                                                                    /organism-"Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
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                                        /clone_lib-"RPCI-11"
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                                                             /clone="RP11-459119"
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                        CATCCTGACTGCACTGGACATCTTTGTGGACCGGCGTGTGTCTGCACTGCCTGTGGTCAA
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Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedis University of Agricultural Sciences, BMC Box 597, Uppsala 751 24,
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Milan, D., Jeon, J.T., Looft, C., Amarger, V., Robic, A., Rogel-Gaillard, C., Paul, S., Gellin, J., Lundstrom, K., Kalm, E., Le Roy, P., Chardon, P. and Andersson, L.
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Sus scrofa AMPK gamma subunit (PRKAG3) gene, complete cds.
AF214521
AF214521.1 GI:8215685
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                                                                                          Conservative
                                                                                                                                                                                                                                       /product="AMF gamma subunit"
/protein_id="AAF73989.1"
/protein_id="AAF73989.1"
/db_xref="Gi:8215686"
/translation="MSFLEOGESRSWPSRAVTTSSERSHGDQGNKASRWTRQEDVEEG
GPPGPREGPQSRPVAESTGQEATFPKATPLAQAAPLAEVUNPPTERDILLESDCAASAS
DSNTDHLDLGIEFSASAASGDELGLVEEKPAPCPSPEVLLPRLGWDDELGKPGAQVYM
HEMQEHTCYDAMTSSKLVIFDTMLEIKKAFFALVANGVRAAPLABDKKQSFVGMLTI
TDFILVLHRYYRSPLVQITEIEEHKIETWREIYLGGCFKFLVSISSNDSLFEAVVALI
KNRIHRLPVLDPVSGAVLHILTHKFLLKFLHIFGTLLPRPSFLXRTIQDLGIGTFRDL
AVVLETAPILTALDIFVDRRVSALPVVNETGQVVGLYSREDVIHLAAQGTYNHLDMNV
GEALRQRFLCLEGVLSCQPHETLGEVIDRIVREQVHRLVUDETQHLLGVVSLSDILQ
ALVLSPAGIDALGA"
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Join(1. 154.515. .918,1809. .1890,2349. .2407,2509. .2554,

2771. .2825,3027. .3153,3286. .3451,4578. .4615,4791. .4937,

5294. .5410)
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<1. .>5410
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/map="15q"
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/db_xref="taxon:9823"
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2896	TGCCCCGCACAGACCCCCTTCTCCAGCTCATCGGTTC	2837	Db
1112	acctgagcctcctcccacagtccccttccccagtcccactcagct	1053	Qy
2836	acctgcaaggctgcttcaagcctctggtctccatctcctaatgataggtgggtg	993 2777	Db Qy
2776	-caaggtgaaggtgaccggccccrrggcctgactctggctctttctgcagagatct 		Оy
933	aca9999a99acaata99a9cctc999tgcct9ac9gaa99gaagctgcct99gactg- 		Db Qy
1 874	GGTGAGGATGGGGCCAAGGACCTCAGGGAGAGCATGCGCAGTGGAGGTTTCCTGGAGGAA	820 2597	Оу
819	agattgagacctggaggggtgagtggggagaggaacccggaaaggggctgttggt	765 2537	Оy
764	tctgacttctggagtcctgtcgatgtctctaggtccagatctatgagattgaacaacata 	705 2477	Оу
704	agaggggcggggggggaggagtcctcctggagcctggtgccctagaagcccacgtctt	645 2440	Оу
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2320	gaggggatctgaccctcaacctgccttccacccaaaggcccgggct	479 2261	Оу
9 478 3 2260	ccactgtcctgttcccacagtccccactgtgtctcagcacaaggacactggcagggtggg 	419 2201	Оу
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      Submitted (17-JAN-2001) Genome Analysis, Institute of Molecular Submitted (17-JAN-2001) Genome Analysis, Institute of Molecular Blotechnology, Beutenberstr. 11, Jena 07745, Germany NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence says soon as it is available and the accession number will
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                                                                                                                                                              Rump,A., Hayes,C., Brown,S.D.M. and Mouse chromosome 1 genomic sequence
                                                                                                                                                                                    Mus musculus
Eukaryota; Metazoa; Chordata;
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
1 (bases 1 to 227724)
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AF336381.1 GI:13507298
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preserved
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Sciurognathi; Muridae; Murinae; Mus
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PAC457, **
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Sequence
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                      Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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/db_xref="taxon:10090"
/chromosome="1"
/clone="pAc510; PAC457"
a 55423 c 56238 g 58199
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1. .227724
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17969: gap of unknown Length
32746: contig of 14777 bp in 1
32846: gap of unknown Length
227724: contig of 194878 bp in
Luthman, H.
                                                                                                                           1647 bp
Patent W00177305.
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Pred. No. 2.3e-40;
0; Mismatches 126;
and
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Marklund
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                          Craniata; Vertebrata; Catarrhini; Hominidae,
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                                        Euteleostomi;
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Sequence 3
Ax099776
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                                                                                   Patent: WO 0120003-A 3 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA)
Andersson, Leif (SE); Looft, Christian (DE); Kalm,
                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2109)
                                                                                                                               same, and uses thereof
                                                                                                                                            Variants of the gamma chain of ampk,
                                                                                                                                                                     Andersson,L., Looft,C., Kalm,E., Milan,D., Rol
Rogel-Gaillard,C., Tannuccelli,N., Gellin,J.,
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serikgrakalrwidoksveegeprogegorspapaesiglatpfyttplaoa
dpagvctpptcwdclesbcTasaagsstdbvelatefpateameceleglleerpal
LSPQAPFPKLGwddelrkpgaQ1Ymrfwoehtcvdamarssklvifdtmleikkapfa
LVANOYRAAPLWDSKKOSFVCHLTITDFILVLHRYYRSPLVOIYEIEOHKIETWREIY
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GSLLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVVNECGQV
VGLYSRFDVIHLAAQQTYNHLDMSVGEALRQRTLCLEGVLSCQPHESLGEVIDRIARE
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/db_xref="taxon:9606"
20. .1489
  /note="unnamed protein product"
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Pred. No. 4.2e-30;
0; Mismatches 8
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tgcactggacatctttgtggaccggcgtgtgtctgcactgcctgtggtcaacgaatgtgg 1689
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INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA)
Andersson, Leif (SE); Looft, Christian (DE); Kalm,
Location/Qualifiers
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Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A., Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       same, and uses thereof
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                        /Translation="MSFLEQENSSSWBSPAYTSSSERIRGKRRAKALRWTRQKSYEEG
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RFWQEHTCYDAMATSKLVIFDTMLEIKAFFALLVANGVRAAPLWDSKKQSFVGMLTI
TDFILVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKPLVSISPNOSLFEAVYTLI
KNRIHRLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDL
AVVLETAPILTALDIFVDRRYSALPYVNECGQVVGLXSRFDVHLAAQQTYNHLDMSV
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YRTIODLGIGTFRDLAVVLETAPIITALDIFVDRRYSALFVVNECGQVYGLYSRFDVI
HLAAQQTYNHLDMSVGEALRQRTLCLEGVLSCOPHESIGEVIDRIAREQVHRLVLVDE
TOHLLGYVSLSDILQALVLSPAGIDALGA*
                                                                                                                                                                                                                                                                                              /note="unnamed protein product"
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Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 2115)
2 (bases 1 to 2115)
3 (bases 1 to 2115)
4 Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Kalm,E., Le,Roy,P., Chardon,P. and Andersson,L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M., Rogel-Gaillard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H., Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               skeletal muscle
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/product="AMP-activated protein kinase gamma subunit"
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1. .2115
                                                                                                                                                                                                                         /map="2p"
                                                                                                                                                                                                                                                                      /organism-"Homo
                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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Clinical Sciences Centre, Hammersmith
London, W12 ONN, UNITED KINGDOM
Location/Qualifiers
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Cheung, P.C., Salt, I.P., Davies, S.P., Hardie, D.G. and Carling, D. Characterization of AMP-activated protein kinase gamma-subunit isoforms and their role in AMP binding
Blochem. J. 346 Pt 3, 659-669 (2000)
                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AMP-activated protein kinase; AMPK gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AMPK gamma 3 gene).
AJ249977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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/evidence-experimental
/product="AMP-activated protein kinase gamma 3 subunit*
/protein_id="Caba5117.1"
/db_xref="GI:6688201"
/translation="MEPGLEHALRRTPSWSSLGGSEHQEMSFLEQENGSSWPSPAVTS
SSERIRGKRRAKALRWTROKSVEEGEPPEQGEGPRSRPAAESTGLEATFPKTTPLAQA
DPAGVCTPPTGWDCLPSDCTASAAGSSTDDVELATEFPATEAMPCELEGLLEERPALC
LSPQAPFPKLGWDDELRKPGAQIYMRFIEEHTCYDAMATSSKLVIFDTMLEIKKAFFA
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ALVLSPAGIDALGA"
a 622 c 562 g 471 t
                                                                                                                                                                                                     /gene="AMPK gamma
22. .1500
                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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KNRIHRLPYLDPYSGNYLHILTHKRLLKFLHIFGSLLPRPSFLYRTIQDLGIGTFRDL
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                                                                                                                                     /codon_start-1
                                                                                                                                                                    /gene-"AMPK gamma 3"
/function-"AMP-activated
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th Hospital, DuCane Road,
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Query Match 8.0
Best Local Similarity 88.0
Matches 160; Conservative
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Matches 173
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173; Conserv
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Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy,P.
Chardon,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1 from Patent WO0120003.
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                                                                                                                                                                                                                                                                                                                         same, and uses thereof
Patent: WO 0120003-A 1 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA)
Andersson, Leif (SE); Looft, Christian (DE); Kalm,
                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; 1 (bases 1 to 1867)
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HLAAQOTYNHLDMNVCBALRORTLCLEGVLSCQPHETLGEVIDRIVREQVHRLVLVDE
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583 c 529 g 375 t
                                                                                                                                                                                                                                                        /organism="Sus scrofa"
/db_xref="taxon:9823"
472. .1389
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LQGCFKPLVSISPNDSLFEAVTLIKNRIHRLPVLDPVSGNVLHILTHKRLLKFLHIF
GSLLPRPSFLYRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVVNRCGQV
VGLYSRFDVIHLAQQTYNHLDMSVGEALRKRTLCLEGVLSCQPHESLGEVIDRIARE
QVHRLVLVDETQHLLGVVSLSDILQALVLSPAGIDPSGPEKI*
a 674 c 617 g 498 t
                                                                                                                                                                                                                                       /note="unnamed protein product"
                                                                                                                                                                                                                            /codon_start=1
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1. .1867
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95.68;
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0; Mismatches
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                 148; DB 6;
No. 3.2e-25;
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1 (bases 1 to 1873)
Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M., Rogel-Gaillard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H., Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, University of Agricultural Sciences, BMC box 597, Uppsala 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 1873)
Milan, D., Jeon, J.T., Looft, C., Amarger, V., Robic, A.,
Rogel-Gaillard, C., Paul, S., Gellin, J., Lundstrom, K.,
Kalm, E., Le Roy, P., Chardon, P. and Andersson, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        skeletal muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A mutation in PRKAG3 associated with excess glycogen content in pig
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Sus scrofa
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Sus scrofa AMP-activated
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             GEALRORTLCLEGVLSCOPHETLGEVIDRIVREQVHRLVLVDETQHLLGVVSLSDILQ
ALVLSPAGIDALGA"
1 580 c 535 g 376 t
                                                                                                                                                                                                                                                                               /note="AMPKG3"
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                                                                                                                                                                                                                                                                                                                                                         /tissue_type="skeletal muscle"
l. .1873
                                                                                                                                                                                                                                                                                                                                                                                              /chromosome="15"
/map="15q"
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/db_xref="taxon:9823"
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Query Match

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160; Conserv
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patent: WO 0120003-A 27 22-MAR-2001;
INSTITUT MATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA)
Andersson, Leif (SE); Looft, Christian (DE); Kalm,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 1873)
Andersson, L., Looft, C., Kalm, E., Milan, D., Robic, A., Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., le Roy, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Variants of the gamma chain of ampk,
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GPGPREGPOSREVAESTGQEATFPKATPLAQAAPLAEVDNPPTERDILPSDCAASAS
DSNTDHLDLGILEFSASAASGDELGLVEEKPAPCPSPEVLLPRLGWDDELQKPGAQVYM
HFWQEHTCYDAMATSSKLVIFOTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLTI
TDFILVLHRYYRSPLVQIYEIEEHKIETWREIYLQGCFKPLVSISPNDSLFEAVYALI
KNRIHRLPVLDPVSGAVLHILTHKKFLHIETHLFFRFLLFRTJQLGTGTFRDL
KNRIHRLPVLDPVSGAVLHILTHKRLKFLHIETTLLFRSFLYRTJQDLGTGTFRDL
AVVLETAPLITAALDIFVDRRVSALPVVNETGQVVGLYSRFDVIHLAAQQTYNHLDMNV
GEALRORTLCLEGVLSCQPHETLGEVIDRIVREQVHRLVLVDETQHLLGVVSLSDILQ
GEALRORTLCLEGVLSCQPHETLGEVIDRIVREQVHRLVLVDETQHLLGVVSLSDILQ
ALVLSPAGIDALGA"
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/db_xref="G1:13538835"
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/db_xref="taxon:9823"
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Best Local Similarity 88.9%;
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patent: WO 0120003-A 31 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA)
Andersson, Leif (SE); Looft, Christian (DE); Kalm,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Cetartiodactyla; Suina; Suidae; 1 (bases 1 to 2022)
Andersson, L., Looft, C., Kalm, E., Milan, D., Robic, A., Rogel-Gaillard, C., Tannuccelli, N., Gellin, J., le Roy
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2000US-0608408.
2000US-0632366.
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The invention relates to a spatially-addressable set of single exon CC nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting CC from human breast and BT 474 cells. The method involves contacting CC the probes with a collection of detectably labelled nucleic acids CC derived from mRNA of human breast, and then measuring the label CC county in the expression of regions of genomic DNA predicted to cerifying the expression of regions of genomic DNA predicted to come code proteins. They are useful for gene discovery, and for CC determining predisposition and/or prognosing breast disease. Gene CC expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater CC agents of probes for measuring gene expression, with far less bias CC than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The Dresent sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this pattent did not form part of the printed specification, but was obtained in electronic format directly considered the production int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful for measuring gene expression in breast, comprises number of single exon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 spatially-addressable set of single exon nucleic acid probes, ful for measuring gene expression in sample derived from human ast, comprises number of single exon nucleic acid probes -
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Sequence

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21-SEP-2000;
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04-OCT-2000;
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26-MAY-2000;
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                                                                                                                                                           GGAGTCTGCATGGCCAGCTGGGAGACCCTGGGGGCTCAATTTCCCCCATCTGTGGAGCCGCT
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Best Local Similarity
Matches 362; Conser
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26 - MAY - 2000;
30 - JUN - 2000;
03 - AUG - 2000;
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27-SEP-2000;
04-OCT-2000;
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GGAGATGGAGGAGGGGGAGATCTTGTACGGTTGTTCTGGGGGCTGATCTCTGATAT
                                         CCCTCTATGGGACAGCAAGAAGCAGAGCTTTGTGGGTGAGGAGAGGCTGGGGAGGTGAAG
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21-SEP-2000;
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04-OCT-2000;
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brains
                                                                                                                                         probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-FEB-2000;
26-MAY-2000;
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probes which are derived from genomic sequences expressed bone marrow. They can be used to measure gene expression i samples, which may enable the improved diagnosis and treat

re gene expression in diagnosis and treatme

in the human in bone marrow

of cancers

analyzing

gene

genome-derived

erived single exon expression in huma

nucleic bone

acid

probes

useful

roj

marrow

Example

SEQ

IJ

20

658pp + human

Sequence Listing;

English nucleic

invention

provides a number of single exon

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RESULT 7
AAA13465/c
ID AA1134
XX AA1134
XX AA1134
XX Probe;
XX Probe;
XX Probe;
XX CCETV1C
XX Homo 9
XX Ho
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26-MAY-2000; 2000US-0008408.
30-JUN-2000; 2000US-0632366.
21-SEP-2000; 2000US-06323659.
21-SEP-2000; 2000US-0234697.
27-SEP-2000; 2000US-023659.
04-OCT-2000; 2000GB-0024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Probe; human; mi
cervical cancer;
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probes of the
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                                                                                MOLECULAR DYNAMICS INC
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                                         Hanzel DK,
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invention
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Pred.
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6.9e-83;
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Query Match
Best Local Similarity 99.7
Matches 362; Conservative
                                                                                                                                                                                                                                                     The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printe specification, but was obtained in electronic format directly from WIPC at fifty.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                       Sequence 378 BP; 80 A; 128 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 25; SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No 3398; 487pp;
                                                                                20.4%;
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                                                    Score 351; DB 22;
Pred. No. 6.9e-83;
D; Mismatches 0
                                                                                                                                                                                                          97 G; 73 T;
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                       agc
                                               atgaccagctgacacctttcacctccgctactgcatggccctgtgccataggtgctaggg
                                                                                                                                                                                                                                                       ccctctatgggacagcaagaagcagagctttgtgggtgaggagaggctggggaggtgaag
                                                                                                  accacaagcttggcttcaggccaagcccagccaggggccagggtggaggaaagtccatcc
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RESULT 8
AAI34821/C
ID AAI34821 standard; DNA; 378
                                                 genetic
                                                       Probe; microarray; human;
                                                                    Probe #3507
                                                                                17-OCT-2001
                                                                                             AAI34821;
                                                 disorder;
                                                                   used
                                                                               (first entry)
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                                                                   measure gene expression in human placenta
                                                      placenta;
                                                       antenatal
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diagnosis

sample

30-JAN-2001; 2001WO-US00663

09-AUG-2001. WO200157272-A2 Homo

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RESULT 9
AAI03344/c
ID AAI03344 standard; D
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AC AAI03344;
XC AAI03344;
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DT 09-OCT-2001 (first
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DE Probe #3335 used to
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26 - MAY - 2000;
30 - JUN - 2000;
03 - AUG - 2000;
21 - SEP - 2000;
27 - SEP - 2000;
04 - OCT - 2000;
                   Probe #3335 used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to single exon nucleic acid probes The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying expression in samples derived from human placenta. The probes are for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
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                                                                                                                                                                                                          99ag1ct9cat9gccagct9g9agaccctggggctcaatttccccatctgtggagccgct
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                                                                                                                                                                                                                                      ACCACAAGCTTGGCCTTCAGGCCAAGCCCAGGCCAGGGCCAGGGTGGAAGGTCCATCC
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2000US-0608408
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2000US-0234687
2000US-0236539
2000US-0236539
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                                                                           DNA;
                   measure gene expression
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cancer;
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04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                          The present invention relates to novel single exon nucleic acid probes because it is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the hybridises at high stringency to a nucleic acid expressed in the breast. The probes are useful for predicting, diagnosing, grading staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic actiology. The disease, include: breast cancer, disorders of development, inflammatory dof the breast, fibrocystic changes, proliferative breast disease.
                                                                                                                                                                                                                                                                Claim
 Sequence
                                              Note: The sequence data for this patent did not form specification, but was obtained in electronic format
                                                                                   non-carcinoma tumours
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                                                                                                                                                                                                                                                                                                                Novel single
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2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-02346859.
2000US-0236359.
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                                            ggagtctgcatggccagctgggagaccctggggctcaatttccccatctgtggagccgct
                                                                                                                                                    accacaagcttggcttcaggccaagcccagccaggggccagggtggaggaaagtccatcc
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Local Similarity

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DB 22; .9e-83;

Length

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ARAO8485
ID Huma
KW Huma
KW Prolin
KW Ctiss
IN Ctiss
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cc sequences ABA08223-ABA09574 represent nucleic acids encoding them. The clivention also relates to vectors and recombinant host cells comprising a cconnucleotide of the invention, methods of producing the novel polypeptides, cc antibodies against the polypeptides, methods of identifying compounds which cor polypeptides in a sample, and methods of identifying compounds which cor polypeptides of the invention. Although novel, many of the cc polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence compounds activities, including cytokine, cell proliferation or cell conferential therapeutic applications. The polypeptides of the invention may differential their activities; stem cell growth factor activity; that commondulatory activity; this growth factor activities; commondulatory activity; activin- or inhibin-related activities; chemotactic or chemokinetic activities; haemostatic, thrombotic or thrombolytic activities; receptor or ligand activities; or may be converted to the invention are useful for preventing, treating or ameliorating medical contention are useful for preventing, treating or ameliorating medical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-FEB-2000; 2000US-0496914.
27-APR-2000; 2000US-0560875.
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cc conditions, e.g., by protein or gene therapy. Such conditions include cc cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell colisorders), chronic inflammatory conditions (e.g., asthma or arthritis), cc disorders), chronic inflammatory conditions (e.g., asthma or arthritis), cc arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal cc vascular growth. Polypeptides involved with tissue regeneration and cc repair (or nucleic acids encoding them) may be used to promote wound the promote wound cc immunomodulatory activities may be used in the treatment of viral, cc immunomodulatory activities may be used in the treatment of viral, cc bacterial and fungal infections in addition to immune disorders. Cc Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to promote cell growth. For example, such polypeptides and nucleotides that can be used to augment or replace cells damaged by illness, can autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug soreal in the collection of the above conditions, and in drug soreal in the collection of the above conditions.
   Sequence 547 BP; 112 A; 172 C;
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95.3%;
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                              "Silent variation"
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No. 7
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RESULT 1
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMP-activated protein kinase gamma 3 subunit (PRRAG3). Detecting a risk estimate of the PRRAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution P1A; in exon 4 variation may be a substitution of a T for a C at nucleotide 530; and in exon 10 variation may be a substitution of a T for a C at nucleotide 137, resulting in the amino acid substitution R340W. There may also be nucleotide variation in intron 6. The numbering of these variations is based on the full length cDNA as given, rather than on position 1 of the open reading frame.
     Human; gamma
                          Human AMPK gamma subunit muscle-specific isoform, PRKAG3 cDNA
                                                                                                                                                                                       1189
                                                           13-JUN-2001
                                                                                        AAD03296;
                                                                                                               AAD03296 standard; DNA; 2109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-657170/75.
P-PSDB; QQB47679.
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nilarity 95.6%;
Conservative
subunit; adenosine monophosphate-activated kinase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  represents the full length cDNA encoding the human protein kinase gamma 3 subunit (PRKAG3). Detecting
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Pred. No. 2.5e
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Query Match Best Local Matches

Similarity 95.0 73; Conservative

9.8%;

Score 168.2; Pred. No. 2.8e 0; Mismatches

.8e-34

Indels Length

Gaps

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Sequence

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470 T;

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cc useful as therapeutic for treating carbohydrate metabolism disorders such cas diabetes, obesity, and disorders associated with muscle metabolism cc such as myopathy and cardiovascular diseases, to modulate AMPK cc activity, and for restoring a normal AMPK function. PRKAG3 sequence called its functionally altered mutants are useful for the diagnostic called to genetic testing and prognosis of a metabolic disorder. Cc preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are cuseful for detecting a dysfunction of carbohydrate metabolism resulting cfrom the expression of a functionally altered allele of PRKAG3. Cc Transgenic animal and host cell transformed with PRKAG3 or a heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid consisting PRKAG3 is useful for detecting mutations in a PrKag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain con PRKAG3 and is useful in gene therapy.
                                                                                                                                                                                                                                                               The present sequence is a cDNA encoding human adenosine monophosphate (AMP) activated kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is
                                                                                                                                                                                                                                                                                                                                               Claim 12; Fig
                                                                                                                                                                                                                                                                                                                                                                                  New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of associated with energy metabolism such as diabetes, obesity,
                                                                                                                                                                                                                                                                                                                                                                           myopathy
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Iannuccelli N,
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18-MAY-2000;
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      The present sequence is a cDNA encoding human adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, complete PRKAG3. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic
evaluation, genetic testing and prognosis of a metabolic
                                                                                                                                         Claim 12; Page 65-68; 71pp; English
                                                                                                                                                                         New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of associated with energy metabolism such as diabetes, obesity,
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Iannuccelli N,
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/product= "Human complete Prkag3 protein"
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INRA INST
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                                                                   99EP-0402236
2000EP-0401388
                                                                                                                                         2000WO-EP09896
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472..1389
/*tag= b
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/product= 1390..1867
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                   NAT RECH AGRONOMIQUE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            adenosine monophosphate activated kinase; besity: myopathy; cardiovascular disease;
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Pred. No. 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disease; anorectic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC (AMP) activated kinase (AMPK) gamma subunit muscle-specific isoform, CC PRKAG3. Prkag3 gene is located in the RN locus of chromosome 15.
CC Mutation in Prkag3 results in an altered regulation of carbohydrate CC metabolism, particularly in skeletal muscle. PRKAG3 is useful as CC diabetes, obesity, and disorders associated with muscle metabolism cC such as myopathy and cardiovascular diseases, to modulate AMPK CC activity, and for restoring a normal AMPK function. PRKAG3 sequence CC and its functionally altered mutants are useful for the diagnostic CC evaluation, genetic testing and prognosis of a metabolic disorder, CC preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3 are CC useful for detecting a dysfunction of carbohydrate metabolism resulting CC from the expression of a functionally altered allele of PRKAG3. CC Transgenic animal and host cell transformed with PRKAG3 or a heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid confined and is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                    PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorec genetic testing; carbohydrate_metabolism disorder; skeletal muscle;
                                                                                                                                                                                                                                                         1029
           cystathione beta synthase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1867
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                                                                                  gamma subunit muscle-specific isoform, complete PRKAG3 cDNA
                                                                                                                                                                             standard;
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N, Gellin
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                                                     adenosine monophosphate-activated kinase;
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         CBS;
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                                     disease; anorectic;
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New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of associated with energy metabolism such as diabetes, obesity,
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(ANDE/)
(LOOF/)
                                                                                                                                                            Claim 12;
                                                                                                                                                                                                          WPI; 2001-244810/25
P-PSDB; AAE00222.
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18-MAY-2000;
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) ANDERSSON L.
) LOOFT C.
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, Gellin
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1..1395
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/product= "Sus scrofa complete Prkag3 protein"
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J, Le Roy P, (
                                                                                                                                                                                                                             n D, Robic
Chardon P;
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CC (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, CC complete prkAG3. PrkAG3 yersel is located in the RN locus of chromosome CC 15. Mutation in Prkag3 gene is located in the RN locus of chromosome CC in the specific for treating carried the specific seriol as CC therapeutic for treating carried results in an altered regulation of carbohydrate CC diabetes, obesity, and disorders associated with muscle metabolism CC such as myopathy and cardiovascular diseases, to modulate AMPK CC activity, and for restoring a normal AMPK function. PRKAG3 sequence CC and its functionally altered mutants are useful for the diagnostic CC evaluation, genetic testing and prognosis of a metabolic disorder, CC preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are CC useful for detecting a dysfunction of carbohydrate metabolism resulting CC in a sequence canimal and host cell transformed with PRKAG3 or a heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid cencoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain CC of PRKAG3 and is useful in gene therapy.

Sequence 1873 ВP; 382 A; 580 C; 535 G; 376 T; 0 other;

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                                                                                              Query Match
Best Local Similarity 88.9
Matches 160; Conservative
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            tttgggcatcggcacattccgagacttggctgtggtgctggagacagcacccatcctgac 1629
                                              tttgggcatcggcacattccgagacttggccgtggtgctggaaacggcgcccatcctgac
                                                                                                          8.6%;
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Pred. No. 5.8e-
D; Mismatches
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tgcactggacatctttgtggaccggcgtgtgtctgcactgcctgtggtcaacgaatgtgg 1689

Db 1035 cgcactggacatcttcgtggaccggcgtgtgtcttgcgctgcctgtggtcaacgaaactgg 1094

Search completed: October 3, 2002, 16:30:16

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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
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Copyright (c) 1993 - 2000 Comp
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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US-08-272-796-14
US-09-272-796-14
US-09-272-796-17
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US-08-466-390-3
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Sequence 63, Appl
Sequence 14, Appl
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Sequence 11, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 11, Appl
Sequence 13, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 3, Appl
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Score 68. Pred. No. ; Mismat	50 14 H, E	US-08-687-080 US-09-155-768 US-08-456-200 US-08-193-078 US-08-193-078 US-08-193-095 US-08-149-097 US-08-163-163 US-08-163-163 US-08-163-163 US-08-163-163 US-08-163-163 US-08-163-163 US-08-163-163 US-08-163-163 US-08-163-163
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DB 3; 9-09; 47;	ts Institute	17777 BE 888881115
Length Indel	Protein Protein	
157 s	n Kina	Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence
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Gaps		115. Appli 1. Appli 18. Appli 8. Appli 8. Appli 8. Appli 8. Appli 19. Appli 10. Appli 11. Appli 11. Appli 11. Appli 12. Appli 13. Appli 14. Appli 15. Appli 17. Appli 17. Appli 17. Appli 18. Appli 19. Appli
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTzqpt-F1s
US-08-232-463-14
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                                                                                                                                                  Ouery Match 3.9%; Score 67.6; DB 1; Length 7218; Best Local Similarity 6.2%; Pred. No. 1.6e-08; Matches 25; Conservative 223; Mismatches 152; Indels 0
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Palent No. 5670367
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMPLECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)836-4109
                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                               906 ctgacggaagggaagctgcctgggactgcaaggtgaggcaggtgaccggctcccctggcc 965
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ZIP: 22313-0299
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CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
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1800 Diagonal Road, Suite 500
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CLONE: 1452972	
; IMMEDIATE SOURCE:	
; TOPOLOGY: linear	
c acid	
LENGTH: 1435 base pai	
: SEDUENCE CHARACTERISTICS: 14:	
TIMEODUATION FOR GEO ID NO. 11.	
TELEFAX: 415-845-4166	
1	
; REFERENCE/DOCKET NUMBER: PF-0321 US	
ION NUMBER: 36,749	
; NAME: Billings, Lucy J J	
APPLICATION NUMBER:	
; PRIOR APPLICATION: 435	
•	
; CURRENT APPLICATION DATA:	
SYSTEM: DOS	
; COMPUTER: IBM Compatible	
: MEDIIM TYPE: Diskette	
94304	
; CITY: PAIO ALCO ; STATE: CA	
STREET: 3174 Porte	
Н	
CORRESPONDENCE ADDRESS: AL	
TITLE OF INVENTION: KINASES	
TITLE OF INVENTION: DISEAS	
APPLICANT:	
APPLICANT: Lal, Preeti	
APPLICANT: Guegler, Karl	
APPLICANT: Corley, Neil C.	
APPLICANT:	
GENERAL INFORMATION:	
; Sequence 14, Application US/U8878989 ; Patent No. 5885803	
989-14	
Db 1378 ΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥ	
Qy 1266 tcatcaagaaccggatccatcgcctgcctgttcttgaccc 1305	
Db 1318 ΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥΥ	
Oy 1206 taggetgeccegaggetcactgetcecatctetgeagectgtttgaagetgtetacacec 1265	
Db 1258 אינימימימימימימימימימימימימימימימימימימי	
Oy 1146 aagggagcottggtgccctgccttcttttaggggcctgggatggaggttgtctctccc 1205	
Db 1198 מינימימימימימימימימימימימימימימימימימימ	
Oy 1086 ccccttccccagtcccactcagctctgaactcacctcttcatcctaggcggcacacagac 1145	
Db 1138 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY	
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US-09-272-796-14
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Best Local Similarity
Matches 89; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1435 base pairs
        STRANDEDNESS: SI
TOPOLOGY: Linear
IMMEDIATE SOURCE:
LIBRARY: PENITUJ
CLONE: 1452972
                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0321 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Shah, Purvi
TITLE OF INVENTION: DISEASE
TITLE OF INVENTION: KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J J
                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/272,796
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                              nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                        94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Incyte Pharmaceuticals, Inc. 
3174 Porter Drive
                                                                                                                                                     415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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Corley, Neil C.
Guegler, Karl G.
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Shah, Purvi
                                                  linear
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Pred. No. 8.8e-08;
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US-08-232-463-14
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US-08-232-463-14/c
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                  Query Match
Best Local s
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                                                                                                                                                                         TELEX: 899149
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/07,
FILING DATE:
APPLICATION NUMBER: EP 91
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                               IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                      NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                629 CAGCTTTTTAT 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         509 AGCCTCTTCGATGCTGTATACTCCTTGATCAAAAATAAAATCCACAGATTGCCCGTTATT
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   Local Similarity 3.6%; nes 13; Conservative
                                                                                                                               TOPOLOGY:
                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                        TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       y Match 3.7%;
Local Similarity 67.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alexandria
                                                                                                                                                          nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                         (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCHEIFLINGER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
3.5%; Score 61; DB 1; Le
3.6%; Pred. No. 9.6e-07;
ive 212; Mismatches 132;
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Pred. No. 8.8e-08;
0; Mismatches 42
                               DB 1; Length 7218;
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Conservative 212;

Indels

0;

Gaps

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Sequence 17, Application US/09007005B
Patent No. 625858
GENERAL INFORMATION:
APPLICANT: Szostak, Jack W.
APPLICANT: Szostak, Jack W.
APPLICANT: Liu, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: FUSIONS
FILE REFERENCE: 00786/350003
CURRENT APPLICATION NUMBER: US/09/007,005B
CURRENT APPLICATION NUMBER: 00/05,963
EARLIER FILING DATE: 1997-01-27
EARLIER FILING DATE: 1997-01-27
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER FILING DATE: 1997-11-06
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: LOCATION: (1)...(289)
: OTHER INFORMATION: n = A,T,C
US-09-007-005-17
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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tgacggaagggaagctgcctgggactgcaaggtgaggcaggtg 949
                                       rnrsrnrnrsrnrnrsrnrnrsrnrnrsrnrnrsrnrnrsrnrnrsrnrnrsrnrnrsrn 202
                                                                        gatgggcagtgggatgtcctggagtgaacaggggagggacaataggagcctcgggtgcc 906
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: LCCATION: (1)...(289)
: OTHER INFORMATION: n = A,T,C or
US-09-244-796-17
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APPLICANT: ROBERTS, RICHARD W.
APPLICANT: LIU, Rihe
APPLICANT: LIU, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNJ
TITLE OF INVENTION: FUSIONS
FILE REFERENCE: 00786/350007
CURRENT APPLICATION NUMBER: US/09/244,796
CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER APPLICATION NUMBER: 09/007,005
EARLIER APPLICATION NUMBER: 09/007,005
EARLIER APPLICATION NUMBER: 09/007,005
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US-09-244-796-17
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Best Local S
Matches 6
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SOFTWARE: FASTSEQ for Windows Version 4.
SEQ ID NO 17
LENGTH: 289
TYPE: RNA
ORGANISM: Artificial Sequence
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Patent No. 6281344
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                                                       APPLICANT: LANDES, GREGORY M
APPLICANT: BURN, TIMOTHY C
APPLICANT: CONNORS, TIMOTHY D
APPLICANT: DACKOWSKI, WILLIAM
APPLICANT: GERMINO, GREGORY
  NUMBER
                  APPLICANT: QIAN, F
TITLE OF INVENTION:
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SEQUENCES:
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                                         QIAN, FENG
                                                                                                                                                                     KLINGER,
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2.7%; Pred. No. 0.16;
                                                                                                                                                                         KATHERINE
                  POLYCYSTIC KIDNEY DISEASE GENE
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                                                                                                                                                                                                                                Sequence 1, Application US/08658136
Patent No. 6071717
GENERAL INFORMATION:
APPLICANT: KLINGER, KATHERINE W
APPLICANT: LANDES, GREGORY M
APPLICANT: BURN, TIMOTHY C
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Best Local :
                                                                                                                                    APPLICANT: CONNORS, TIMOTHY D
APPLICANT: DACKOWSKI, WILLIAM
APPLICANT: GERMINO, GREGORY
APPLICANT: QIAN, FENG
TITLE OF INVENTION: POLYCYSTIC
NUMBER OF SEQUENCES: 58
                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 508-872-5415 INFORMATION FOR SEQ ID NO:
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                       CORRESPONDENCE ADDRESS:
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TELECOMMUNICATION INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOUTWARE: PALENTIA Release #1.0, Version
CURRENT APPLICATION DATA:
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ADDRESSEE: GENZYME CORPORATION
                                                                       STREET: ONE MOUNT
CITY: FRAMINGHAM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,845
                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 508-872-8400
TELEFAX: 508-872-5415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/658, 136
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                                                              MASSACHUSETTS
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                                                                                                          GENZYME CORPORATION
Floppy disk
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                                                                                                                                         POLYCYSTIC KIDNEY DISEASE GENE 58
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Pred. No. 1.7;
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); Mismatches
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US-09-165-264-7
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                                                                                                                                                                                                                                                                              SOFTWARE:
SEQ ID NO 7
                                                                                                                       Matches
                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/09165264 Patent No. 6197510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 52.1%; Matches 87; Conservative
                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-872-5400
TELEPAX: 508-872-5415
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                 LENGTH: 320
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                     SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
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897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                 126
                                                                             777 ggaggggtgagtggggagaggaacccggaaaggggctgttggtgatggtgatgggccagggct 836
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TOPOLOGY: lin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
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                                                          ctcgggtgcctgacggaagggaagctgcctgggactgcaaggtgagg 943
                                                                                                                       95;
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IVENTION: Multi-Loci Genomic Analysis
:NCE: 44747
                                                                                                                     Conservative
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 0.27
0; Mismatches
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                                                                                                                                  DВ
. 27;
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                                                                                                                                               Length 320;
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Length 319;

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CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
LENGTH: 319
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                   RESULT 12
US-09-165-264-8
Sequence 8, Application US/09165264
Patent No. 6197510
GENERAL INFORMATION:
: OTHER INFORMATION: Description of Artificial Sequence:Primer sequence US-09-165-264-8
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; OTHER INFORMATION: Description of Artificial Sequence:Primer sequence
US-09-165-264-14
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CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity
                                                                                                                                                                        APPLICANT: Vinayagamoorthy, Thuraiayah TITLE OF INVENTION: Multi-Loci Genomic Analysis FILE REFERENCE: 44747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
OKGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 320
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RESULT 14
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; OTHER INFORMATION: Description of Artificial Sequence:Primer sequence
US-09-165-264-13
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US-09-165-264-13
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Sequence 11, Application US/09165264
Patent No. 6197510
GEMERAL INFORMATION:
APPLICANT: Vinayagamoorthy, Thuraiayah
TITLE OF INVENTION: Multi-Loci Genomic Analysis
FILE REFERENCE: 44747
CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/165,264
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13, Application US/09165264 Patent No. 6197510 GENERAL INFORMATION:
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Best Local :
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
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VENTION: Multi-Loci Genomic Analysis
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Pred. No. 1.2;
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Pred. No. 0.56;
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RESULT 15
US-07-959-943-6/c
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SUPTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 320
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence:Primer sequence
US-09-165-264-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/07959943
Patent No. 5418162
GENERAL INFORMATION:
APPLICANT: Blakely, Randy D.
APPLICANT: Fremeau Jr., Robert T.
APPLICANT: Caron, Marc G.
TITLE OF INVENTION: Serotonin Transporter cDNA
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 87
                                                                            TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2278 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: single
                                                                                                                                                                      ATTORNEY, AGENT INFORMATION:
ATTORNEY, AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5405.38a
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
FEATURE:
                              MOLECULE TYPE: CDN
POSITION IN GENOME:
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ADDRESSEE: Gibson
STREET: Post Office Drawer 31:
CITY: Raleigh
STATE: No. 5418162th Carolina
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               UNITS:
                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                APPLICATION NUMBER: UPFILING DATE: 19921014 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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VTRY: U.S.A.
27622
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11 Similarity 50.68;
87; Conservation
            2278 basepairs
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                                               CDNA
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2.1
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; LOCATION:
US-07-959-943-6
                                                                                                                                                          Query Match 2.1
Best Local Similarity 51.9
Matches 81; Conservative
1823 TTCAGGAGTGATACTTTTAATAATGCGCTCCTTAAG 1788
                                                  1883 TCCCAGGGTGTTACACAGCATTCATGCGGATGTCCCCCACACGGGATTTCTGTGGGTGT
                                                                                                     1943 GGGGAGGAGTCCAGTGGGGCTTTTCAGAGCTGAGAGAGGTGGCTGGGAAGAGGTGTCCTC 1884
                731 ctctaggtccagatctatgagattgaacaacataag
                                                                671 tcctggagcctggtgccctagaagcccacgtctttctgacttctggagtcctgtcgatgt 730
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48..1868
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Pred. No. 3;
0; Mismatches
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Search completed: October 3, 2002, 16:18:58 Job time: 16778 sec

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Result
No.
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Maximum
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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DB
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Match Length DB
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length: 2000000000
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Gapop 10.0 , Gapext 1.0
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gb_htg:*
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em_on:*
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Variants of the human amp-activated protein kinase gamma 3 subunit
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Location/Qualifiers
/Organism="Homo sapiens"
/Ob_xref="taxon:9606"
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Chemistry: Dye-primer ET; 98% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 187795 bases at least 040
Consensus quality: 190513 bases at least 030
Consensus quality: 192099 bases at least 030
Consensus quality: 192099 bases at least 020
Insert size: 200000; agarose-fp
Insert size: 194954; sum-of-contigs
Quality coverage: 5.58 in 020 bases; sum-of-contigs
Ouality coverage: 5.57 in 020 bases; sum-of-contigs
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                                                                                                                                             * NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (08-JUN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Feb 21, 2001 this sequence version replaced gi:8469048.
                                                                                                                                                                                                                                                                                                                                                                                                       Web site:http://genome.wustl.edu/gsc/index.shtml
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be preserved.
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                                                                                   /note="assembly_name:Contig32" 149388. .196554
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92241. .113337
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73917, .92140
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113438. .130325
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/note="assembly_name:Contig21"
11957. .15783
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28988. .35255
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/db_xref="taxon:9606"
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5 (bases
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Submitted (03-JAN-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                      Direct Submission
Submitted (08-NOV-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
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Homo sapiens BAC clone RP11-459119
AC009974
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6 (bases 1 to
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Submitted (08-SEP-1999) Genome
University School of Medicine,
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4 (bases 1 to
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Center project name: H_NH0459I19
          Contact: sapiens@watson.wustl.edu
                                                  Center: Washington University Genome Sequencing Center Center code: WUGSC
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted

> all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >-30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc Louis

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu)
VECTOR: pBACe3.6 one male Frengen,E.,

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-1077K22; the clone sequenced to the right is RP11-647O5. Actual start of this sequenced to the right is RP11-459I19; actual end is at base position 1 of RP11-459I19. clone

AC009974. Polymorphisms have been identified between AC073128 and AC009974. A single plasmid region exists beteen 38812-38903. Am unresolved tandem in the HERV SVA exists between 184390-185163. PCR suggests that approximately 1700 bps are missing.

FEATURES misc_feature source /note=' /note= /note=' 164. /note="similar to Homo sapiens EST BI114348 (NID:g14565249)" /note="match /note-"match /note="match /note="match note-"match /note="match /note=*match to /note="match /note="match to /clone_"RP11-459I19" /clone_lib="RPCI-11" /db_xref="taxon:9606" /chromosome="2" note="match to EST BI059713 (NID:g14467240)" /note="match to EST BE314060 (NID:g9134719)" organism="Homo sapiens" .206854 -"match to 221 match match ť ç 6 ç to EST ç б ő ť EST BF304755 (NID:g11251653)" EST BF183086 BE908408 A1670836 BE908408 (NID:g10402954)" BG477625 (NID:g13409904)* BE047599 BG470047 C05773 (NID:g1502549)* BE047599 (NID:g8364652) tz39c01.y1" AW880850 AL567345 (NID:g10402954)" (NID:g8364652) tz39c01.y1* (NID: g13402322)" (NID:g4850567) wa04g10.x1" (NID: 98042860)" (NID: 912920610) (NID: g11061273)"

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Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J. C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lakoqque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, J., Meneus, L., Mihova, T., Miranda, C., Menga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T. M., Oliver, J., Peterson, K., Pierre, N., O'Neil, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Stange, Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: sequence_submissions@genome.wi.mit.edu
Insert size:
Insert size:
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85023 contig of 7807 bp in length

85023 contig of 7807 bp in length

85123 gap of 100 bp

85123 gap of 100 bp

93315 93414: gap of 100 bp

93415 101193: contig of 7779 bp in length

101194 101293: gap of 100 bp

101294 113090: contig of 11797 b-

113091 113190: gap of 11797 b-

113191 133190: gap of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is
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be preserved.
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123497 123596: gap of
123597 137837: contig
137838 137937: gap of
                                                                                                                                                                                                                                                                                                                                                                                          66596 66695; gap of 100 bp
66696 73218; contig of 6523 bp in length
73219 73318; gap of 100 bp
73319 77115; contig of 3797 bp in length
73716 77215; gap of 100 bp
77316 77215; gap of 100 bp
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3 2502: gap of 100 bp
1 3823: contig of 1321 bp in length
3923: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15143: gap of 100 bp
17123: contig of 1980 bp in length
17223: gap of 100 km
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                                                                                       113090: contig of 11797 bp in length
3190: gap of 100 bp
123496: contia of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185: gap of 100 bp
55871: contig of 4486 bp in length
371: gap of 100 bp
60595: contig of 4624 bp in length
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42366: contig of 4087 bp in length
66: gap of 100 bp
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38179: contig of 4111 bp in length
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183: gap of 100 bp
12556: contig of 2473 bp in length
156: gap of 100 bp
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19466: contig of 2243 bp in length
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35: contig of 5900 bp in length
gap of 100 bp
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Query Match Best Local Similarity Matches 100; Conser	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature		misc_feature	misc_reature	isc_reacur	en fostur	ויי	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature	misc_feature			FEATURES * 137938
98.4%; Score 99.4; DB 2; ity 99.0%; Pred. No. 1.2e-16; servative 0; Mismatches 1;	/note="assembly_iragment" 101294113090 /note="assembly_fragment"	fragment	<pre>"assembly_fragment .93314</pre>	assembly_fragment.85022	assembly_fragment	y_fragment	-"assembly_tragment 66595	y_fragment	ragment	651285	y_11	, '-	.38179	.33968 assembly f	2716030170 "- 'note="assembly fragment"	lęr i	.24319 assembly f	.21928 assembly	ft"	.19466 assembly_fra	/note="assembly_fragment"	/note="assembly_fragment"		<pre>/note="assembly_fragment" 10084</pre>	/note="assembly_fragment" 76489983	<pre>/note="assembly_fragment" 62627547</pre>	te="assembly_f 16161	agment	, ;	•	fragment "	man ма]⊖	/Organism="Homo sapiens" /Ab vrof="tayon:0606"	38 152129: contig of 14192 bp in Location/Qualifiers
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Best Local Similarity
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                                                                   62 aggggagtcctcctggagcctggtgccctagaagcccac 100
                                                                                                                                                                              61
                                          GGGGAAGCCCTCCAGGAGCCGGGGAAGGAGGCGGCCCAC 2084
                                                                                                                                               59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Premont, R.T., Koch, W.J., Inglese, J. and Lefkowitz, R.J. Roch, W.J., Inglese, J. and Lefkowitz, R.J. Identification and characterization of GRK5, a member of the family of G protein-coupled receptor kinases J. Biol. Chem. 269, 6832-6841 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (02-SEP-1993) Richard T. Premont, Department of Medicine, Duke University Medical Center, Durham, NC 27710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus
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Bos taurus GRK5 protein kinase mRNA,
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                                                                                                                                                                                                                                                                                                                                                                                                                          673
                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="GRK5 protein kinase"
/product="GRK5 protein kinase"
/protein_id="AAA17561.1"
/db_xref="GI 437106"
/db_xref="GI 437106"
/translation="MELENIVANTVLLKAREGGGGKRKGKSKKWKEILKFPHINGCED
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KKRIKKRKGESMALNEKQILEKVNSRFVVNLAYAYETKDALCLVLTIMNGGDLKFHIY
NMGNPGFEEERALFYAAEILCGLEDLHHENIVYRDLKFERNILLDDYGHIRISDLGLAV
KIPEGDLIGGRVGTYGYMAPEVLNNORYGLSDDYMGLGCLIYEMIEGQSPFRGRKEKV
KREEVDRRVLETEEVYSHKFSEEAKSICKMLLTMDAKQRLGCQEEGAAEVVRHPFFRN
MNTKRLEAGMLDPFYPDPRAVYCKDYLDIEGFSTVKGVNLDHTDDDFYSKFSTGSVP
                                                                                                                                                                                                                                                                                                                                                                                                                                              IPWQSEMIETECFKELNVFGPHGTLSPDLNRSHPPEPPKKGLLQRLFKRQHQNNSKSSPNHSTNSKTSFNHHINSNHVSSNSTGSS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /evidence=experimental
/product="GRK5 protein
175. .1947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="tongue epithelium"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Bos taurus"
/db_xref="taxon:9913"
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                                                                                                                                                                                                                                                                                   34.78;
                                                                                                                                                                                                                                                                                   Score 35;
Pred. No.
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                                                                                                                                                                                                                                                                                                             4; Length 2539;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL Submitted (21 NoV-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 29, 2000 this sequence version replaced gi:9863492.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Mp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr13 RP11-264J4 is from the library RPCI-11.1 constructed at the Roswell Park Cancer Institute by the group of Pleter de Jong. For further details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                             IMPORTANT: This sequence is not the entire insert of clone RP11-264J4 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true right end of clone RP11-264J4 is at 127794 in this sequence. The true left end of clone RP11-501K3 is at 100168 in this sequence. The true right end of clone RP11-110K18 is at 21477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human DNA sequence from clone RP11-264J4 on chromosome 13. Contains STSs, GSSs and CpG islands. Contains the 3' part of the ZNF198 gene for zinc finger protein 198, a novel gene, a gene for novel connexin (gap junction protein), a novel cyclophilin type peptidyl-prolyl cis-trans isomerase pseudogene and the GJB2 gene for gap junction protein beta 2, 26 kD (connexin 26), complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL138688.27 GI:9944124 HTG; connexin; CpG island; cyclophilin; gap junction protein; GJB2; prolyl cis-trans isomerase; zinc finger; ZNF198.
                                                                                                                                                                                                                                                                                                                                                                                                               in this sequence.
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                              /note-"AluY repeat: matches 1. .294 435. .508
/note-
                                                                                                          /note="AluJ/FLAM repeat: matches 1.
                                                                                                                                                             /note="AluJ/FLAM repeat: matches 2. .69 of consensus"
                                                                                                                                                                                                             /clone="RP11-264J4"
/clone_lib="RPCI-11.1"
                                                                                                                                                                                                                                                                              /chromosome="13"
                                                                                                                                                                                                                                                                                                                             ∕organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                            1. .127794
                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9606"
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                                                                                          . 371
  L1MB3 repeat: matches 6109.
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  .6181 of consensus
                                                        of consensus"
                                                                                                             .69 of consensus
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                                                                                                                                                                                                                                                                                                                  Em:(14) 1472 Em:(AF)(1812 Em:(AF)(1812 Em:(AF)(1812) Em:(A
                                                                                                                                                                                                                                                                /evidence=not_experimental 7550. .12268
                /note="continues in ball0K18 (AL137119) match: proteins: Tr:043308 Tr:Q9UBW7 Tr:043434 Tr:060898 Tr:Q9VB55 Sw:Q14202"
                                                                                                                                              /gene="ZNF198"
join(<7550. .7664,8315. .8566,9190.
/gene="ZNF198"
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/note="LIMEc repeat: matches 2194...2318 of consensus"

6026 ...6319
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Em:Y13472 Em:AB002383 Em:AF161582 Em:X95808
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/note="MER38 repeat: matches 5. .57 of consensus
MER58 repeat: matches 5. .57 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4573. .4877
/note-"Alusc repeat: matches 1. .306 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4202. .4434
/note="MER33 repeat: matches 44. .324 of consensus
MER33 repeat: matches 44. .324 of consensus"
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3251. .3534
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/note="AluSx repeat: matches 43. .311 of consensus"
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1208. .1524
                                                                                                                                                                       .9310,11356.
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GGGGGCATCCCGCAG 44384
                                                                                                                                                                  Conservative
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12268
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//note="match: GSS: Em:AQ142889"
16151. 16285
/note="MER46C repeat: matches 181. .333 of consensus
MER46C repeat: matches 181. .333 of consensus"
16354. 16432
/note="MER46C repeat: matches 2 . .81 of consensus
MER46C repeat: matches 2 . .81 of consensus
MER46C repeat: matches 2 . .81 of consensus"
                                                                                                                                                                                                                                                                                                                                     /note="L2 repeat: matches 2668.
17564. 17668
                                                                                                                                                                                                                                                                                                                                                                                                                    /note="L2 repeat: matches 2641.
complement(16918. .17359)
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                                                                                                                                                                                                                                                    183161. .18307
/note="MIR repeat: matches 6. .174 of consensus"
18633. .18949
                                                                                                                                                                                                                                                                                              /note="MER5A repeat: matches 57. .161 of consensus"
18161. .18307
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12662. .12957
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17228. .17305
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12269. .12338
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9552. .9843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="YLCGSNRKDNIFIDPGYOTFEGELNKILRSWOPSILPDGSIFSR
VEEDYLWRIKGLGSH5PVALLWTLFYFWTKYFGLKTVEGHLLLSGGTVFRHWKKNPLT
MENKACLRYQVSSLCGTDNEDKITTGARKHEDDEPVFEGIENTANPSRCPVKMFECYL
SKSPQNLNQRMDVFYLQPECSSSTDSPVWYTSTSLDRNTLENMLVRVLLVKDIYDKDN
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10438. .10804
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/product="bA26474.1 (zinc finger protein 198)"
/protein_ida="cac16956.1"
/db_xref="GI:11322768"
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                                                                                                                                                                                    34.78;
                                                                                                                                                            Score 35; DB 9; Pred. No. 6.3; 0; Mismatches :
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TITLE
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                                                                                                                                         Gallus gallus
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 895)
1 (bases 1 to 895)
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47; Conserv
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AF461698
                 GenBank staff at the National Library of Medicine created this entry [NCBI glbbsq 144347] from the original journal article.
                                                              The expression pattern of the chick homeobox role in patterning of the limbs and face and compartmentalization of somites pev. Biol. 161 (2), 357-369 (1994)
                                                                                                                                                                                                                                              chicken heart stage 17 embryo.
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$69088
$69088.1 GI:545359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (21-DEC-2001) Otolaryngology, University of Florida, 12901 Bruce B. Downs Blvd., Tampa, FL 33612,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Venkataramu, C.R. and Sokolowski, B.H.A. Protein protein interactions of Kvbeta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Archosauria; Aves; Neognathae; Phasianinae; Gallus.
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                                                                                                                                  Olson, E.N.
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/Codon_Start=1
/product="paired-related homeobox"
/protein_id="mal67846.1"
/protein_id="mal67846.1"
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SSQUQALERVFERTHYPDAFVREDLARRVNLTEARVQVWFQNRRAKFERNEEAMLASK
SSQUQALERVFERTHYPDAFVREDLARRVNLTSARVQVWFQNRRAKFERNEEAMLASK
NASLLKSYSGDVTAVEDPIVPRPAPRTDYLSWGTASPYSAMATYSTTCTNASP"
a 220 c 217 g 97 t
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/db_xref="taxon:9031"
/tissue_type="inner ear"
/dev_stage="embryonic"
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67.1%;
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Pred. No. 59;
0; Mismatches
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Gallus gallus p
D13433
D13433.1 GI:22
                                                                                                                                                                                                                                                                       Submitted (20-OCT-1992) Tsutomu Nohno, Kawasaki Medical School, Dept. of Molecular Biology; 577 Matsushima, Kurashiki, Okayama 701-01, Japan (Tel:0864-62-1111(ex.3637), Fax:0864-62-1199) L (bases 1 to 1084)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      paired-related homeobox Gallus gallus (library: clones p2 and p7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 Similarity
47; Conserv
                                                                                                                                                                                         A chicken homeobox gene related to Drosophila paired predominantly expressed in the developing limb Dev. Biol. 158 (1), 254-264 (1993)
                                                                                                                                                                                                                                          and Noji, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus gallus
                                                                                                                                                              Submitted (20-OCT-1992) to DDBJ by:
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                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                             Department of Pharmacology
                                                                                                                                              Tsutomu Nohno
                                                                                                                                                                                93321789
                                                                                                                                                                                                                                                                                                                                           Direct Submission
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                                             Phone:
                                                                               Kurashiki 701-01
                                                                                                577 Matsushima
                                                                                                            kawasaki Medical School
                                                                                                                                                                                                                                                           Nohno, T.,
                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 1084)
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255 c 246 g 140 t
               Location/Qualifiers
                                                                                                                                                                                                                                                         Koyama, E., Myokai, F., Taniguchi, S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAB29880.1"
/db_xref="GI:545360"
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/note="homeobox"
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.1084
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Ohuch1, H.,

Saito, T

cDNA to

mRNA,

Euteleostomi;

VRT 03-FEB-1999

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Gaps

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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10
                                                                                                                                                            Submitted (02-AUG-1996) Osamu Ohara, Kazusa DNA Research Institute; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:comlainfo@kazusa.or.jp, Tel:+81-438-52-3913)
                                                                                                                                                                                                                                                                                                        Nagase,T., Seki,N., Ishikawa,K., Ohira,M., Kawarabayasi,Y., Ohara,O., Tanaka,A., Kotani,H., Miyajima,N. and Nomura,N. Prediction of the coding sequences of unidentified human genes. V The coding sequences of 80 new genes (KIAAO201-KIAAO280) deduced analysis of cDNA clones from cell line KG-1 and brain DNA Res. 3 (5), 321-329 (1996)
                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                          2 (bases 1 to 6335)
Ohara,O., Nagase,T., Kikuno,R. and Nomura,N.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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/cell_type="myeloblast"
/tissue_type="bone marrow"
                                                                       /organism⇒"Homo sapiens"
/db_xref⇒"taxon:9606"
/chromosome⇒"chromosome 6.
/clone="HA2570"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
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/product"/paide-related homeotic gene product"
/protein_ide=BAA02695.1"
/protein_ide=BAA02695.1"
/db_xref="GI:222851"
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AGDMYAAQGDEGGEGEGRESLLESPGLTSGSDTPQQDNDQLNSEEKKKRKQRRNRTTFN
SSQLQALERVFERTHYPDAFVREDLARRVNLTEARVQYWFQNRRAKFERNERWLASKN
ASILKSYSGDVTAVEQDIVPRPAPRPTDYLSWGTASPYSAMATYSTTCTNASPAQGMN
                                                        /sex="male"
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233. .967
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/db_xref="taxon:9031"
/clone_lib="lambda gt10"
/dev_stage="Stage 24-26"
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Chlamydomonas reinhardtii
Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
Center: Department Of Chemistry And Biochemistry
The University Of Oklahoma
                                                                           OK 73019, USA on Jan 29, 2002 this sequence version replaced g1:16271941
                                                                                                                                    Submitted (02-JUN-2001) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
                                                                                                                                                                                                Jia,H., Lin,S., Wu
Direct Submission
                                                                                                                                                                                                                                                                                                               1 (bases 1 to 54018)
Jia, H., Lin, S., Wu, H., Dutcher, S. and Roe, B.A.
Chlamydomonas reinhardtii BAC Clone cr-4121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chlamydomonas reinhardtii clone cr-4i21, WORKING DRAFT SEQUENCE, 5
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/codon_start=2
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                                                                                                                                             OK 73019,
On Jan 29,
 * NOTE: This is a 'working draft'
* consists of 4 contigs. The true
* is not known and their order in
                                                                                    Center: Department Of Chemistry And Biochemistry
The University Of Oklahoma
                                                                                                                                                                   Direct Submission
Submitted (21-FEB-2001) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
                                                                                                                                                                                                                          Wu,H., Lin,S., Jia,H., Dutcher,S. and Roe,B.A.
                                                                                                                                                                                                                                                                                  1 (bases 1 to 65898)
Wu.H., Lin,S., Jia,H., Dutcher,S. and Roe,B.A.
Chlamydomonas reinhardtii BAC Clone cr-32m22
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/db_xref~"taxon:3055"
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5117: gap of unknown length
10018: contig of 4901 bp in length
10118: gap of unknown length
21786: contig of 11668 bp in length
21886: gap of unknown length
3146: contig of 11260 bp in length
33246: gap of unknown length
54018: contig of 20772 bp in length.
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                                       Submitted (04-APR-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 ISA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Mar 26, 2000 this sequence version replaced gi:7327699.

IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known; 800 n's separate contig_ID; 00404 Length: 157824bp

Contig_ID; 01411 Length: 1050bp.

**NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

**This record will be updated with the finished sequence will be preserved.

**Boon as it is available and the accession number will
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161999 bp DNA linear HTG 04-A
HOMO sapiens chromosome 10 clone RP11-411B6, *** SEQUENCING
PROGRESS ***, 3 unordered pieces.
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Mammalia; Eutheria;
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4554: gap of unknown length
18724: contig of 14170 bp in le
18824: gap of unknown length
30657: contig of 11833 bp in le
30757: gap of unknown length
65898: contig of 35141 bp in le
157824: contig of 157824 bp in length
3624: gap of 800 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC097417/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39337 CTGATGAAGACTAGGCGGGGGCAAGGCTGTGGCACCAGATGGGCAGGGGTGCTGGGGAGG 39396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39397 CCAAAAGTAACCAGCTTCCCTCCAAAC 39423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
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                     Benton, J., Binage, K., Blankenburg, K., Banks, T., Barbaria, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carrer, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy, Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwalte, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Harris, C., Harris, K., Harris, M., Haylak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Jackson, L. E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Louiseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Martinez, E., Massey, E., Mawhiney, E., Metced, M., Martindale, A., Morris, S., Moser, M., Neal, D., Newtson, N., Judies, A., Nguyen, N., Nguyen, N., Nguyen, N., Neal, D., Newtson, N., Owledo, R., Pace, A., Payton, B., Peters, L., Pickens, R., Primus, E., Pul, L., Oulles, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Saerks, A., Sparks, A., Stalley, H., Shooshtari, N., Stserks, A., Stalley, H., Shooshtari, N., Stalley, H., S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                al Similarity
53; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Raltus norvegicus clone CH230-201C5, ***, 69 unordered pieces. AC097417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HTG; HTGS_PHASE1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Norway rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC097417.3 GI:17973606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 172748)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            158625 160139: contig of 1515 bp in length 160140 160939: gap of 800 bp 160940 161999: contig of 1060 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
Savery,G., Scherer,S., Scott,G., Shen,H., Shooshta, Sodergren,E., Sonaike,T., Sparks,A., Stanley,H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="RP11-411B6"
/clone_lib="RPCI-11.2"
35796 c 36927 g 43
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .161999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HTG 20-DEC-2001
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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    * arbitrary. Gaps between the contigs are represented as 
* runs of N, but the exact sizes of the gaps are unknown. 
* This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Assembly program: Phrap; version 0.990329First call to findPhrapList
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (18-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plazza, Houston, TX 77030, USA
On Dec 20, 2001 this sequence version replaced qi:17064486.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R. Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wieczyk, R., Wooden, S., Watlington, S., Williams, G., Williamson, A., Wieczyk, R., Wooden, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., T. Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Wasquez, L., Vera, V., Villalon, D., Vera, V., Vera, V., Vera, V., Villalon, D., Vera, V., V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Consensus quality: 140460 bases at least Q40 Consensus quality: 148273 bases at least Q30 Consensus quality: 155031 bases at least Q30 Estimated insert size: 140848; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 2.1x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 172748)
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STS Content:
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Finishing Completed at Stanford Human Genome Center
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Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 203200)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                       Quality: Phrap Quality >=40 99.5% of Sequence;
Estimated Total Number of Errors is 0.8.
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On Jan 22, 2001 this sequence version replaced gi:11178043
Draft Sequence Produced by DOE Joint Genome Institute
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Eukaryota; M
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Homo sapiens chromosome 19 clone CTD-2561020, complete sequence.
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Copyright (c) 1993 - 2000 Comp
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Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being part and is derived by analysis of the total score distribution. being printed,

SUMMARIES

3683 3683 1253 9253 9549 9549 9549 1154
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Human herpesvirus		HSV-2 strain SB5 C	HSV-2 strain SB5 C	Human reproductive	Human adenosine re	ໝ	Human adenosine re	Human low adenosin	Human immune/haema	immune/haem	used	#3021	Probe #2909 for ge	Human bone marrow	brain	: #2926 for g	foetal	_	Human colon cancer	immun	CDNA	Human ATFx coding	cancer asso	CDNA c	immune,	#22880 used	#1615	bone m	brain expre	#17409	Human foetal liver	bone	bone	an bone ma	DNA encoding novel

ALIGNMENTS

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RESULT
PRKAG3 intron 4 - intron 10
                                  21-JAN-2002 (first entry)
                                                                     AAH43683;
                                                                                                        AAH43683 standard; DNA; 1722 BP
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Human; AMP-activated protein kinase gamma 3 subunit; P metabolic disease; diabetes; obesity; substitution; ds PRKAG3; variant;

Homo sapiens.

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AAH43683
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                                                                                                                                                  The sequences given in AAH43681-84 represents genomic fragments encoding the human AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution P71A; in exon 4 variation may be a substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution R340W. There may also be nucleotide variation
                                                                                                                           Sequence 1722 BP;
                                                                                                                                                                                                                                                                                Example 1; Fig
                                                                                                                                                                                                                                                                                                          New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and method for determining a risk estimate of diseases in subject by detecting the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   portion of intron
                                                                        0;
                                                                      Score 101; DB 22;
Pred. No. 1.3e-18;
; Mismatches 0;
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                                                                                                                           G;
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                                                                                                                           other;
                                                                       Indels
                                                                                          Length 1722;
                                                                     0;
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ABA61253
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ABA6
AC AB
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                                                                                                RESULT
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Best Local
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
ABA29092
                                             ABA29092 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 9558; 639pp + sequence listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200157277-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JAN-2001; 2001WO-US00669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human foetal liver single exon nucleic acid probe
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                                                                                                                                                                                                  cctcctggagcctggtgccctagaagc
                                                                                                                                                                  ccaaaagtaaccagcttccctccaaac
                                                                                                                                                                                                                                                                        ctgatgaagactaggcgggggcaaggctgtggcaccagatgggcaggggtgctggggagg
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                                                                                                                                                                                                                                                                                                                                                                                1 Similarity 53; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0180312

2000US-0207456

2000US-0608408

2000US-0632366

2000US-05323687

2000US-0236359

2000US-0236359

2000US-0236359
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                                                                                                                                                                                                                                                                                                                                                                                                32.3%;
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                                             ВP
                                                                                                                                                                                                                                                                                                                                                                           Score 32.6; DB Pred. No. 4.3; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                0,
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RESULT
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Best Local
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26 - MAY - 2000;
30 - JUN - 2000;
03 - AUG - 2000;
21 - SEP - 2000;
                                                                                                                                                                                                                                                                                                                     The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular systems. Cardlovascular disease, hypertension, cardiac arrhythmias and
          05-NOV-2001
                                                    AAK09549 standard;
                                AAK09549;
                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
                                                                                                                                                                                                                                                                                                     Note:
                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ
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04-OCT-2000;
                                                                                                                                                                                                                                                                                        specification,
                                                                                                                                                                                                                                                                                                              congenital heart disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human: gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   hearts
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                                                                                                            245
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ecification, but was obtained in electronic fo
ftp.wipo.int/pub/published_pct_sequences.
                                                                                                          ccaaaagtaaccagcttccctccaaac 271
                                                                                                                       cctcctggagcctggtgccctagaagc
                                                                                                                                                 ctgatgaagactaggcgggggcaaggctgtggcaccagatgggcaggggtgctggggagg
                                                                                                                                                              2001-488899/53
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                                                                                                                                                                                                                                                         550
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2000US-0207456
2000US-0608408
2000US-0632366
2000US-0234687
2000US-02346359
2000US-0236359
                                                                                                                                                                                                  Conservative
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         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                          ID No 7558;
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                                                     DNA;
                                                                                                                                                                                                           32.3%;
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                                                     550
                                                                                                                                                                                                                                                                                                                                                                                                                         530pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        probes for analyzing gene expression in
                                                                                                                                                                                               Score 32.6; D
Pred. No. 4.3;
0; Mismatches
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.3;
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RESULT
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26 - MAY - 2000;
30 - JUN - 2000;
03 - AUG - 2000;
                 Homo sapiens.
                                            Human; bone
                                                                Human bone marrow
                                                                                   06-NOV-2001
                                                                                                                       AAK35441 standard; DNA; 550
                                                                                                                                                                                                                                                                                                                        The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                 Single
brains
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27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         epilepsy; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    microarray; Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human brain expressed single
                                                                                                                                                                       245
                                                                                                                                                                                                            185
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                                                                                                                                                                                                                                                           Local
                                                                                                                                           G
                                                                                                                                                                                                        cctcctggagcctggtgccctagaagc
                                                                                                                                                                     ccaaaagtaaccagcttccctccaaac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                SG,
                                                                                                                                                                                                                                                   53; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                          exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             brain expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULAR DYNAMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO:
                               marrow expressed exon; gene expression analysis; probe; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0024263.
                                                                                                                                                                                                                                                  Conservative
                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                 BP;
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                                                                                                                                                                                                                                                                                                154 A;
                                                              expressed single
                                                                                                                                                                                                                                                          32.3%;
                                                                                                                                                                                                                                                                                                                                                                                           9540; 650pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen
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                                                                                                                                                                                                                                                                                                139 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exon; gene expression analysis; probe; disease; multiple sclerosis; schizophrenia;
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                                                                                                                        ВP
                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                          Score 32.6; D
Pred. No. 4.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exon
                                                                                                                                                                                                                                                                                                 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rank DR;
                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        for analyzing gene expression
                                                                                                                                                                                       96
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                                                              exon
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                                                              probe SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ
                                                                                                                                                                                                                                                                    DB
                                                                                                                                                                                                                                                                                                T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ID
                                                                                                                                                                                                                                                 34;
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WO200157276-A2

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Best Local S
Matches 53
04 - FEB - 2000;
26 - MAY - 2000;
30 - JUN - 2000;
03 - AUG - 2000;
21 - SEP - 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                  probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of
                                                                                              WO200157278-A2
                                                                                                                                   cervical cancer;
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 550
                                                         30-JAN-2001;
                                                                            09-AUG-2001
                                                                                                                 Homo
                                                                                                                                                                                  12-OCT-2001
                                                                                                                                                                                                    AAI17045;
                                                                                                                                                                                                                      AAI17045
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27-SEP-2000;
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30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            present invention provides a number of single exon nucleic
                                                                                                                                                                                                                                                                                                                 sapiens
                                                                                                                                                                                                                                                                                                         ctgatgaagactaggcggggggcaaggctgtggcaccagatgggcaggggtgctggggggg
                                                                                                                                                                                                                                                                              ccaaaagtaaccagcttccctccaaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001-488900/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SG,
                                                                                                                                                           #6978 for gene expression analysis in human cervical cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genome-derived single exon nucleic acid probes useful zing gene expression in human bone marrow -
                                                                                                                                          human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                             l Similarity 60.9
53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULAR
                                                                                                                                                                                                                      standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO:
2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-063234687.
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-02346359.
2000US-0236359.
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                                                        2001WO-US00670
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DK,
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                                                                                                                                                                                                                                                                                                                                                                                                                invention.
                                                                                                                                                                                                                      DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9998; 658pp + Sequence Listing;
                                                                                                                                                                                                                       550
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0; Mismatches
                                                                                                                                                                                                                       ВP
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                                                                                                                                                                                                                                                                     271
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                                                                                                                                                                                                                                                                                                                                                      No. 4.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DR;
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RESULT
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                                                                                                                                   04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
  Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genetic disorder;
                                              (MOLE-)
                                                                                                                                                                                                                                                                              30-JAN-2001;
                                                                                                                                                                                                                                                                                                                            09-AUG-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Probe; microarray; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probe #9840 used to measure gene expression in human placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAI41154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAI41154 standard; DNA; 550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Penn
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04-OCT-2000;
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53; Conserv
                                           MOLECULAR DYNAMICS INC.
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Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID No 6978; 487pp;
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                                                                                     2000US-0180312.
2000US-0207456.
2000US-0609408.
2000US-0632366.
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2000US-0236359.
2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                              2001WO-US00663
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2000GB-0024263.
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Chen W,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        placenta;
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Pred. No. 4
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Rank DR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antenatal diagnosis
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Best Local S
Matches 53
     31 - JAN - 2000;
04 - FEB - 2000;
04 - FEB - 2000;
02 - MAR - 2000;
16 - MAR - 2000;
17 - MAR - 2000;
17 - MAR - 2000;
19 - MY - 2000;
07 - JUN - 2000;
07 - JUN - 2000;
07 - JUL - 2000;
07 - JUL - 2000;
11 - JUL - 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; immune; haematopoietic; immune/haematopoietic antigen; cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human
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zing gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immune/haematopoietic
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     2000US-0179065
2000US-018628
2000US-0186350
2000US-0189874
2000US-0199076
2000US-0199123
2000US-0199123
2000US-0205515
2000US-0216866
2000US-0216647
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2000US-0217496
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                                                                                                                                                                                                                                                                                                                                                                                                                           therapy; vaccine; metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA;
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60.9%;
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Pred. No. 4.3;
O; Mismatches
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2000US - 0229513
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2000US - 0241786
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2000US-0225267.
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2000US-0225270.
2000US-0225447.
2000US-0225757.
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2000US-0226681
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05-DEC-2000;
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05-DEC-2000;
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17-NOV-2000;
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17-NOV-2000;
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17-NOV-2000;
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17-NOV-2000;
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                                                                                                                                                                                        acids encoding
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2000US-0256719
2000US-0251479
2000US-0251856
2000US-0251869
2000US-0251869
2000US-0251989
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2000US - 0249207
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2000US-0246611.
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2000US-0246532.
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                                                                                                                                                       NO 31449; 3071pp + Sequence Listing; English
                                                                                                                                                                                                                                       SCI INC
                                                                                                                                                                               human immune/hematopoietic antigen polypeptides, diagnosing and/or treating cancers and
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amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic cattivity, and can be used in gene therapy and vaccine production. (I) composed in polynucleotides may be used in the prevention, diagnosis and creates associated with inappropriate (I) expression. For composed AAK54951 to AAK64702 encode the human immune/haematopoietic antigen

Sequence 680 BP; 116 A; 213 C; 185 G; 166 T; 0 other;

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The invention relates to isolated polynucleotide (I) and C polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The C polynucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques (CI). (II) is useful if or to treat disease states involving CC (II). (II) is useful if or generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical company of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. C disorders forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences. AAS64197-AAS94564 represent novel human CC diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed consecution, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                    biodiversity
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23-AUG-2000;
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56; Conser
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2000US-0649167
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58.9%;
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Pred. No. 4.3;
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RESULT 10
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polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human
                                                                                                                                                                                   The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromo and gene mapping, and in recombinant production of (II). The
                                                                                                                                                                                                                                                             Claim 1; SEQ ID No 9861; 103pp; English
                                                                                                                                                                                                                                                                                                                      diagnostics,
                                                                                                                                                                                                                                                                                             biodiversity
                                                                                                                                                                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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23-AUG-2000;
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2000US-0649167
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medical imaging; diagnostic; genetic disorder;
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RESULT 11
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836666
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Best Local S
Matches 54
                                                                                                                                     Ford JE, and J, and F, and P,
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19-JUL-2000;
03-AUG-2000;
The present sequence is one or an incompanies and the expressed in the bone marrow. The polynucleotide and the polypeptide encoded by it are useful in the treatment of various immune deficiencies and disorders. The deficiencies and disorders may immune deficiencies and disorders may immune deficiencies.
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19-OCT-2000;
30-NOV-2000;
                                                                 Claim
                                                                                  21-JAN-2000;
25-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                        Human; bone marrow; antiinflammatory; cytostatic; neuroprotective; antiviral; antibacterial; antifungal; anti-HIV; haemostatic; immunosuppressive; gene therapy; cytokine cell proliferation; cell differentiation modulator; immune disorder; infection; cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the specification, but was obtained in electronic format directly at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                     P-PSDB; AAM00988
                                                                                                                                                                                              (HYSE-)
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                                                                                                                                                                                              HYSEQ INC.
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                                                                 Page 574-579;
                                                                                                                                                             Boyle BJ,
Mang J, Wer
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2000US-0662191.
2000US-0693036.
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2000US-0620312.
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2000US-0552317
                                                                                                                                                               Werhman
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60.0%;
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D; Mismatches
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Pred. No. 5.
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le AJ, Yan
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RESULT 12
AAH90056/c
1D AAH9000
XX AAH900
XX AAH900
XX Human
XX Human:
KW Human:
KW Inmuno
KW Cell d
KW Inmuno
XX Homo s
XX Ho
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JAN-2000;
25-APR-2000;
09-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; bone marrow; antiinflammatory; cytostatic; neuroprotective; antiviral; antibacterial; antifungal; anti-HIV; haemostatic; immunosuppressive; gene therapy; cytokine cell proliferation; cell differentiation modulator; immune disorder; infection; cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infection, or may result from an autoimmune disorder, a coagulation disorder (e.g. haemophilia), inhibition of tumour cell proliferation, suppression of an inflammatory response or treatment of a nervous system disorder such as Alzheimer's disease. Detection of the presence or increased expression of the polynucleotide or the protein it encodes is useful for the diagnosis and/or prognosis of one or more types of cancer. The polynucleotide and polypeptide can be used as nutritional sources or supplements and in the screening of chemical compounds as potential drugs.
                                                          Novel bone-marrow-expressed polynucleotides and polypeptides, for treating e.g. cancer and immune deficiency disorders
                                                                                                                                                                                                                                                                                                      (HYSE-)
                                                                                                                                                                                                                                                                                                                                                     30-NOV
                                                                                                                                                                                                                                                                                                                                                                                              03-AUG-2000;
14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W0200153453-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                             19-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH90056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAH90056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    573 CCAAAAGTAACCAGCTTCCCTCCAAAAGCA
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                                                                                                                                                                                                                d JE,
e Wang
ehr
                                                                                                                                         2001-488707/53.
DB: AAM00937.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cctcctggagcctggtgccctagaagccca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bone marrow cDNA, SEQ ID NO: 300.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunodeficiency virus; HIV;
                                                                                                                                                                                                                                                                                                                                                  -2000;
-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
54; Conser
                                                                                                                                                                                                                                                                                                      HYSEQ INC
                      Page
                                                                                                                                                                                                      Boyle BJ, Tang
Wang J, Werhman '
Zhou P, Drmana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3889 BP; 861 A; 1090 C; 1008 G;
                                                                                                                                                                                                                                                                                                                                                2000US-0488725.

2000US-0552317.

2000US-0598042.

2000US-06520312.

2000US-0653450.

2000US-0653450.

2000US-0653191.

2000US-0693036.

2000US-0593036.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                           Drmanac RT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antiinflammatory;
                                                                                                                                                                                                                               Tang Y
hman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3892
                                                                                                                                                                                                                                                  YT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 32.4; D
Pred. No. 5.4;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                               u C,
                                                                                                                                                                                                                                                  C, Asundi V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 autoimmune disorder;
                                                                                                                                                                                                                               Xue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99
                                                                                                                                                                                                                            AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             930 T; 0 other,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DΒ
                                                                                                                                                                                                                          Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            infection; cancer;
sorder; haemophilia;
                                                                                                                                                                                                                                                  Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                       Zhang
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                                                                                                                                                                                                                          ŗ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             574
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RESULT 13
AAH89943/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local 9
                                                                                                                                                        09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
          WPI; 2001-488707/53
P-PSDB; AAM00824.
                                              Zhao
                                                                     Ford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expressed in the bone marrow. The polynucleotide and the polypeptide encoded by it are useful in the treatment of various immune deficiencies and disorders. The deficiencies and disorders may be genetic, may be caused by a viral (e.g. HIV), bacterial or fungal infection, or may result from an autoimmune disorder, a coagulation disorder (e.g. haemophilia), inhibition of tumour cell proliferation, suppression of an inflammatory response or treatment of a nervous system disorder such as Alzheimer's disease. Detection of the presence or increased expression of the polynucleotide or the protein it encodes is useful for the diagnosis and/or prognosis of one or more types of cancer. The polynucleotide and polypeptide can be used as nutritional sources or supplements and in the screening of
                                                                                                                                                                                            21-JAN-2000;
25-APR-2000;
                                                                                                                     30-NOV-2000;
                                                                                                                                                                                                                                                                                WO200153453-A2
                                                                                              (HYSE-)
                                                                                                                                 14-SEP-2000;
19-OCT-2000;
                                                                                                                                                                                                                                  23-DEC-2000;
                                                                                                                                                                                                                                                        26-JUL-2001.
                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                         immunosuppressive; gene therapy; cytokine cell proliferation; cell differentiation modulator; immune disorder; infection; c
                                                                                                                                                                                                                                                                                                                                                                                                       Human bone marrow cDNA, SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAH89943;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH89943 standard;
                                                                                                                                                                                                                                                                                                                                                                   antiviral; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        633 CTGATGAAGACTAGGCGGGGGCAAGGCTGTGGCACCAGATGGGCAGGGGTGCTGGGGAGG
                                    ωF,
οQA,
                                 d JE, bu,
o F, Wang J, we
o OA, Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present sequence is one of 251 novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCAAAAGTAACCAGCTTCCCTCCAAAAGCA 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cctcctggagcctggtgccctagaagccca 99
                                                                                                                                                                                                                                                                                                                               immunodeficiency virus;
                                                                                                                                                                                                                                                                                                                                                                                bone
                                                                                             HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3892 BP; 860 A; 1091 C; 1009 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               compounds as potential drugs.
                                                                    Boyle BJ,
                                                                                                                   2000US-0488725.
2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0652450.
2000US-0653450.
2000US-0693036.
2000US-0593036.
                                                                                                                                                                                                                               2000WO-US34960
                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                          Werhman
                                              Drmanac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA; 4886
                                                     Tang YT, L.
                                                                                                                                                                                                                                                                                                                                                               antiinflammatory; cytostatic; neuroprotective;
erial; antifungal; anti-HIV; haemostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32.1%;
60.0%;
                                               RŢ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
                                                        Liu C, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                              autoimmune disorder; haemophilia; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32.4;
No. 5
                                                                                                                                                                                                                                                                                                                                                                                                        74
                                                                    Asundi V,
                                                        Ę,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       932 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
                                                        Yang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polynucleotides
                                                        Chen
Y, z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                     æ
                                                                                                                                                                                                                                                                                                                                          cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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AC ABA7
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AC ABA7
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DT 01-1
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DE Hum
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KW Hum
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OS HOM
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PR 04-
PR 04-
PR 21-
PR 03-
PR 21-
PR 27-
PR 27-
PR 27-
PR 27-
PR 27-
PR WP:
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AND
DR WP:
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AND
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Best L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                  Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human fetal liver -
                                                                                                                                                                                                                                                     04-OCT-2000;
                                                                                                                                                                                                                                                                               21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                            03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         infection, or may result from an autoimmune disorder, a coagulation disorder (e.g. haemophilia), inhibition of tumour cell proliferation, suppression of an inflammatory response or treatment of a nervous system disorder such as Alzheimer's disease. Detection of the presence or increased expression of the polynucleotide or the protein it encodes is useful for the diagnosis and/or prognosis of one
                                                                                                                                                                                                                                                                                                                                                                              04-FEB-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               encodes is useful for the diagnosis and/or prognosis of one or more types of cancer. The polynucleotide and polypeptide can used as nutritional sources or supplements and in the screening chemical compounds as potential drugs.
                                                                                                                                                                                                   (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200157277-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABA73753;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4886 BP; 1117 A; 1370 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expressed in the bone marrow. The polynucleotide and the polypeptide encoded by it are useful in the treatment of various immune deficiencies and disorders. The deficiencies and disorders may be genetic, may be caused by a viral (e.g. HIV), bacterial or fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABA73753 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCAAAAGTAACCAGCTTCCCTCCAAAAGCA 1527
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                                                                                                                                                 Hanzel
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2000US-0207456.
2000US-0608408.
2000US-06323687.
2000US-0234687.
2000US-0234687.
2000US-0236359.
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Matches 52
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                Claim
                                                                                                                                                                                                                                                                                                                                Human; gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.
                                                                                                                                                                                                                                                 30-JAN-2001;
                                                                                                                                                                                                                                                                     09-AUG-2001.
                                                                                                                                                                                                                                                                                        WO200157274-A2
                                                                                                                                                                                                                                                                                                            Homo sapiens.
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mes 52; Conserv
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ted specification, but was obtained in electronic
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                                                                                                                                            MOLECULAR DYNAMICS INC
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                                                                                                                       Hanzel
                                                                              nucleic
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2000US-0207456.
2000US-0608408.
2000US-0632366.
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                                                No 17409;
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The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart, present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derive

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Search completed: October Job time: 14288 sec
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                                                                                                                                                                                                                                                                                                                                                                              from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at (tp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                          Sequence 231 BP; 54 A; 57 C; 63 G; 57 T; 0 other;
                                                                                                                                                              146 ctgatgaagactaggcgggggcaaggctgtggcaccagatgggcagggggtgctggggagg 205
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AL530561 AL530561
B1960536 HVSMEn002
AA872225 oh71b02.s
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BE600794 PI1_90_C0
BE598429 PI1_90_C0
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AG083214 PAR trog1
B1951430 HVSME1002
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                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                  ORGANISM
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                                                                        CE 1 (bases 1 to 682)

Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Chin,A., Begum,D.,

Frisch,D., Atkins,M., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons
,J., Oates,R. and Main,D.

Development of a genetically and physically anchored EST resource
for barley genomics: Morex rachis cDNA library

Contact: Wing RA
Contact: Wing RA
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 654 6293
Fax: 864 654 6293
Email: rwing@clemson.edu
Total hq bases = 121
Seq primer: AATTAACCTAAAGGG
High quality sequence start: 2
High quality sequence stop: 553.
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                                                                                                                                                                                                                                                                                 (normal) Hordeum vulgare
B1960023
B1960023.1 GI:16311278
EST.
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Spermatophyta; Magnoliophyta;
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682 bp mRNA linear EST 22-OCT-2001
HVSMEn0022008f Hordeum vulgare rachis EST library HVcDNA0015
(normal) Hordeum vulgare cDNA clone HVSMEn0022008f, mRNA sequence.
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/clone="HVSMEn0022008f"
/clone_lib="Hordeum vulgare rachis EST library HVcDNA0015
(normal)"
/tissue_type="Rachis"
                                          /organism="Hordeum vulgare"
/cultivar="Morex"
                                                                   Location/Qualifiers
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BE295054
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BE1767103
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yta; Liliopsida; Poales; Poaceae; Pooidea
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A0162755 AU162755
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AL514039 AL514039
AL514251 AL514251
AZ52770 ENTDAR8TF
BF685935 602140240
A1087063 oy70d09,x
BE906990 601499803
BG481234 602528560
BE019039 bb46b11,y
BE250790 601105983
BC294571 601176144
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                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
                                                                                                                                       Plate: LLCM380 row: p column: 01 High quality sequence stop: 687.
                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 833)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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BE559614
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601347308F1 NIH_MGC_8 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
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Mammalia; Eutheria; Primates;
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ilarity 60.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders Also
see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)*
a 262 c 174 g 171 t
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                       /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           above. For more details on library preparation and
/clone="IMAGE:3688176"
                                                                                                               Location/Qualifiers
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Pred. No. 47;
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KEYWORDS SOURCE

VERSION ACCESSION

COMMENT

REFERENCE

TITLE AUTHORS

FEATURES

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                                                                                                                                                                                                                                                                                                          and -minmatch 12 options. PCR PRimers
                                                                                                                                                                                                                                                                                                                                            Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -min:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 377)
Smith, T.P. L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Smith, T.P. L., Grosse, White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                     Plate: 142 row: D column: 8 Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                              FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Smith TPL
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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12477 MARC 2BOV Bos taurus cDNA 5',
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/note="Vector: pCMV SPORT6; Site_1: xbaI; Site_2: xhoI; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas,
                                                                                                             /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-*Organ: lymph; Vector: pOTB7; Site_1: xho1: Site_2: ECORI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/Xho1 sites using the following 5; adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).*
                                                                  /tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                    Location/Qualifiers
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/lab_host="DH10B (phage-resistant)"
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Pred. No. 74;
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Best Local S
Matches 59
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TITLE
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                     ACGKGGKGGACKGKG
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                                                                                                      GGGCAGGAGKGGAAGAKKKGCKGCKGCCCAAGAGKGGCKGGGGKGCAKGGGCKCCA 437
                                                                                                                       aggggagtcctcctggagcctggtgccctagaagcccac 100
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9;
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                                                                                                                                                                                                                                                                                                                g)
                                                                                                                                                                                                                                                                                                          vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com a 189 c 337 g 38 t 113 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                       was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              adrenal, and
a 119 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
/clone="CS0DD007Y022"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="neuroblastoma cells"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex-"male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="LTI_NFL001_NBC4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ∕organism⊷"Homo sapiens"
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59.68;
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                                                                                                                                                                                  Score 33; DB
Pred. No. 2.4e
l3; Mismatches
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99 g 59 t
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                                                                                                                                                                       DB 9; L. 2.4e+02; 23;
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76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Development of a genetically and physically anchored EST resource for barley genomics: Morex rachis cDNA library Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hq bases = 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Wing RA
Clemson University Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Chin,A., Frisch,D., Atkins,M., Yu,Y., Henry,D., Palmer,M., Ra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldea
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                                                                                                                                           114
                                                                                                                                                                                                                                                                                             /note="vector: pBluescript sk(-); Site_1: EcoRI; Site_2: xhoI; plants were grown at Washington State University, Pullman, WA in a greenhouse, the rachises were excised and frozen in liquid nitrogen (Kleinhofs lab). In the TJ Close lab at the University of California, Riverside total RNA was prepared, poly(A) was purified, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript sk(-) cDNA phagemids (Chin). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Box equence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and
                                                                                                                                http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Alsc see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)* 215 c 229 g 8 t
                                                                                                                                                                                                                                                                                      sequence analysis see
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/db_xref="taxon:4513"
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                                  32.5%;
58.0%;
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             Score 32.8; DB 10
Pred. No. 2.6e+02;
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                   66 gagtcctcctggagcctggtgccctagaagcccac 100
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Insert Length: 874 Std Error: 0.00
Seq primer: -40ml3 fwd. Er from Amersham
High quality sequence stop: 230.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 282)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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oh71b02.sl NCI_CGAP_Kid5
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AA872225
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                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                              (Pharmacia), digested with Not I and cloned into the Not I and Econed into the Not I and Econed into the Not I and Econed into the Not I see that the Score is the modified pT773 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo. * 107 c 71 g 55 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapicns"
/db_xref="taxon:9606"
/clone="IMAGE:1472427"
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                                                                                                                                                   32.3%;
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Pred. No. 2.7e+02;
0; Mismatches 39;
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comparison of the body sapiens cDNA clone IMAGE:1472427 3',
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PM4-CI0154-151100-001-h12 CI0154
BF808916
                                          BF808916.1
Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CGAP/BTGAP), Tumo
Unpublished (1998)
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National Cancer Institute / National Institute of N
Disorders and Stroke, Brain Tumor Genome Anatomy Pr
(CGAP/BTGAP), Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AW026388 354 bp mRNA linear EST 09-MAR-2000 wv12f05.xl NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2529345 3'similar to contains element MSR1 repetitive element;, mRNA
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High quality sequence stop: 338.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bonaldo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
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Mammalia; Eutheria;
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                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AW026388.1 GI:5879918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Preparation: M. Bento Soares,
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                                                                                                                                                                                                                                                                                                  /clone-"IMAGE:2529345"
/clone_lib-"NCI_CGAP_Brn23"
/tissue_type="glioblastoma (
/lab_host-"DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                 Score 32.6; DB 9;
Pred. No. 2.7e+02;
0; Mismatches 15
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                                                                    Homo sapiens cDNA,
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                                                                  mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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RESULT
AL585199
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KEYWORDS
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        AUTHORS
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATAGCCCATGCAGCCATGCAGCCTTGCAGCCCAGG
                                                                                                                                                                                                                                                                                    AL585199 mRNA linear EST 28-1
AL585199 BP Chicken Embryo Library Gallus gallus cDNA clone
ROS020D01, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dias Neto,E., García Correa,R., Verjovski-Almeida,S., Briones,M.R., Ragai,M.A., Barcía, Costa,F.F., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                    Gallus gallus
                                                                                      Archosauria; Aves; Neognathae; Phasianinae; Gallus.
                                                                                                       Eukaryola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                    AL585199.1 GI:13163932
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Seq primer: puc 18 forward
                                                                                                                                                                                                   chicken.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: asimpson@ludwig.org.hr
     Chicken Embryo Library
                                                            (bases 1 to 685
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            // note-*Organ: colon_ins; vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.*
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/db_xref="taxon:9606"
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Pred. No. 2.8e+02;
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Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                  Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton,R.D., Oates,R. and Main,D.

Development of a genetically and physically anchored EST resource for barley genomics: Morex unstressed seedling shoot cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 Similarity
46; Conserv
                                                                                                                        Email: rwing@clemson.edu
                                                                                                                                                                                                                                         Clemson University
                                                                                                                                                                                                                                                                Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                 Unpublished (2001)
On Feb 22, 2001 this sequence version replaced gi:13109940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BG309093 735 bp mRNA linear EST 22-OCT-2.
HVSWEc0002B16f Hordeum vulgare seedling shoot EST library
HVcDNA0003 (Etiolated and unstressed) Hordeum vulgare cDNA clone
                                                                                                 Total hq bases = 300
                                                                                                                                                                                                                                                                                                  Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldea
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Roslin, Midlothian, EH25
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
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Contact: Frazer Murray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HVSMEc0002B16f, mRNA sequence.
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/dev_stage="5 days old"
/lab_host="70H10B"
/note="Vector: pBLUESCRIPT SK; Site_1: Not1; Site_2: Sall;
/note="Vector: pBLUEScript Sk; Sit
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/db_xref="taxon:9031"
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Pred. No. 3.
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ed. No. 3.6e+02;
Mismatches 24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              619 TTGGGTGGGTGTGGGCCCC 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              559 CTGGTGGGCAGGGGGGGGGGGGGGGGGGGAGCCGACCGGGGCGTGAGCGGAAGGGAGT 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70
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Department of Botany
The University of Georgia
Plant Sciences Building, Rm.
                                                                                             Contact: Cordonnier-Pratt MM
                                                                                                                               Unpublished (2000)
                                                                                                                                                  An EST database from Sorghum:
                                                                                                                                                                                                          Cordonnier-Pratt, M.-M., Gingle, A., Dean, R., Sudman, M. and Pratt
                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Sorghum.

1 (bases 1 to 382)
                                                                                                                                                                                                                                                                                                                                                                sorghum.
Sorghum bicolor
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50; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                           BE600720.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         00720 382 bp mRNA linear EST 18-AUG-2000
_91_G10.b1_A002 Pathogen induced 1 (PII) Sorghum bicolor cDNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/projects/barley. To order see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/gypages/bgn/31/cover.html)*

89 a 156 c 264 g 116 t 10 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Close laboratory at the University of California, Riverside (Choi, Cose, Fencon). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xhol; Seeds were surface sterilized then germinated under axenic conditions in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref."taxon:4513"
/clone="HbrshEc0002B16f"
/clone_11b-shEc0002B16f"
/clone_11b-shEc0002B10f"
/clone_11b-shEc0002B10F1
/hycDNA0003 (Eriolated and unstressed)"
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/cultivar="Morex"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="Seedling shoot"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GI:9855905
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 32; DB 10
Pred. No. 4e+02;
0; Mismatches
   2502, Athens, GA 30602-7271, USA
                                                                                                                                                  pathogen-induced plants
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103 TGATGATGTGGGGGGGGGGCGCATGCGCAGGCGCAGGAGGAGGAGGCGAGAG 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54;
                                               The University of Georgia Plant Sciences Building, I Tel: 706 542 1860
Fax: 706 542 1805
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
                                                                                                                                                                     Contact: Cordonnier-Pratt MM
                                                                                                                                                                                           An EST database from Sorghum: pathogen-induced plants Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                       Sorghum bicolor
                                                                                                                                              Department of Botany
                                                                                                                                                                                                                                                                    Cordonnier-Pratt, M.-M., Gingle, A., Dean, R., Sudman, M. and Pratt
                                                                                                                                                                                                                                                                                        Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: Liliopsida: Poales: Poaceae: PACC clade: Panicoideae: Andropogoneae: Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA sequence.
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Email: mmpratt@uga.edu
Sequences have been tr
                                                                                                                                                                                                                                                                                                                                                                                                                                                             BE600139.1 GI:9855212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: JEN REV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _79_G07.b1_A002 Pathogen induced 1 (PI1) Sorghum bicolor cDNA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RNA was prepared from infected leaves harvested from 45 seedlings 48 hours after inoculation. Note: young seedlings (2 weeks old) exhibit juvenile resistant reaction, which is an incompatible interaction. As they grow older (4 weeks or older), plants resume susceptibity to anthracnose disease. The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Pathogen induced 1 (PII)"
/note="Organ: Anthracmose infected leaves from
two-week-old sorghum plants 48 hr after inoculation;
Vector: pBluescript II from Lambda Zap II; Site_1: XhoI;
Vector: pBluescript II from Lambda Zap II; Site_1 XhoI;
Site_2: EcoRI: Two-week-old sorghum plants (ETX 623
cultivar) were infected with pathogen (isolate FRM421 of
Colletotrichum graminicola, which is a sorghum isolate).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the pathogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequenced were prepared by mass excision. WARNING: While most or all ESTs are expected to derive from the host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plant, no effort was made to eliminate ESTs deriving from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Sorghum bicolor"
/db_xref="taxon:4558"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 31.8; DB IU;
Pred. No. 4.2e+02;
""smatches 37;
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                                                                                               2502,
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                                                                                               30602-7271, USA
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Best Local Similarity
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                                                                                                                                      Department of Botany
The University of Georgia
Plant Sciences Building, Rm.
                                                           Email: mmpratt@uga.edu
Sequences have been tr
                                                                                                                                                                                                                                                                                                                 clade; Panicoideae; Andropogoneae;
l (bases 1 to 474)
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                                                                                                                                                                                                                                                                                                                                                                            Sorghum bicolor
Eukaryota; Viri
                                       below Phred quality
                                                                                                                                                                                                          Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                             Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence
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primer: JEN REV
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706 542 1805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Pathogen induced 1 (PII)"
/note="Organ: Anthracnose-infected to the very from two-week-old sorghum plants 48 hr after inoculation;
Vector: pBluescript II from Lambda Zap II; Site_1: XhoI;
Vector: pBluescript II from Lambda Zap II; Site_1: XhoI;
Site_2: EcoRI; Two-week-old sorghum plants (BTX 623
cultivar) were infected with pathogen (isolate FRM421 of Collectrichum graminicola, which is a sorghum isolate).
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/db_xref-"taxon:4558"
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16. The
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Pred. No. 4.3e+02;
0; Mismatches 37;
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                                to exclude PolyA, vector and regions threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  induced 1 (PI1) Sorghum bicolor cDNA,
                                                                                                                                            2502,
                                                                                                                                                                                                                                                 pathogen-induced plants
                                                                                                                                                                                                                                                                                       Dean, R., Sudman, M. and Pratt
                                                                                                                                          Athens,
                                                                                                                                                                                                                                                                                                                                Sorghum.
                                                                                                                                          GA 30602-7271,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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REFERENCE
AUTHORS
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BE600794/c
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ORIGIN
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54;
                                                                                                   Email: mmpratt@uga.edu
Sequences have been tri
below Phred quality 16.
                                                                                                                                                                       The University of Georgia Plant Sciences Building, Rm. Tel: 706 542 1805
                                                                                                                                                                                                                                                              Contact: Cordonnier-Pratt MM
Department of Botany
                                                                                                                                                                                                                                                                                                       Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.
                      POLYA-No.
                                                           Seq primer: JEN REV
                                                                                                                                                                                                                                                                                                                                                                    Cordonnier-Pratt, M.-M., Gingle, A., Dean, R.,
                                                                                                                                                                                                                                                                                                                                                                                             clade; Panicoideae; Andropogoneae;
1 (bases 1 to 487)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sorghum bicolor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA sequence.
BE600794
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                                        High quality sequence stop: 486
                                                                                                                                                                                                                                                                                                                         An EST database from Sorghum: pathogen-induced plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sorghum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BE600794.1 GI:9855769
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cultivar) were infected with pathogen (isolate FRM421 of Colletotrichum graminicola, which is a sorghum isolate). RNA was prepared from infected leaves harvested from 45 seedlings 48 hours after inoculation. Note: young seedlings (2 weeks old) exhibit juvenile resistant reaction, which is an incompatible interaction. As they grow older (4 weeks or older), plants resume susceptiblity to anthracnose disease. The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision. WARNING: While most or all ESTs are expected to derive from the host plant, no effort was made to eliminate ESTs deriving from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib-"Pathogen induced 1 (PII)"
/note-"Organ: Anthracnose infected laves from
/note-"Organ: Anthracnose infected laves from
two-week-old sorghum plants 48 hr after inoculation:
Vector: pBluescript II from Lambda Zap II: Site_1: x
Site_2: EcoRI; Two-week-old sorghum plants (BTX 623
Site_2: EcoRI; Two-week-old sorghum plants (BTX 623)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the pathogen.
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/db_xref="taxon:4558"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31.5%;
                                                                                                   trimmed to exclude PolyA, vector and regions 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 31.8; DB 10;
Pred. No. 4.3e+02;
0; Mismatches 37;
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                                                                                                                                                                                                                   30602-7271, USA
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bicolor cDNA,
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SOURCE
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AUTHORS
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BE595429/c
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Best Local Similarity
Matches 54; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
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                                                                                                                                                                              Email: mmpratt@uga.edu
Sequences have been trimmed
below Phred quality 16. The
                                                                                                                                                                                                                                                                                      The University of Georgia Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2000)
Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                               An EST database from Sorghum:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade; Pantcoldeae; Andropogoneae; Sorghum.

1 (bases 1 to 532)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BE595429 532 bp mRNA linear EST 18-AUG-2000 PIL_55_D02.bl_A002 Pathogen induced 1 (PI1) Sorghum bicolor cDNA,
                                                                                                                                                                                                                                                       Tel: 706 542 1860
Fax: 706 542 1805
                                                                                                                                                                                                                                                                                                                                                   Department of Botany
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cordonnier-Pratt, M.-M., Gingle, A., Dean, R., Sudman, M. and Pratt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE595429.1 GI:9850502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BE595429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence.
                                                                                                                                     Seq primer: JEN REV
                                                                                            POLYA=No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84 a
                                                                                                               quality sequence stop: 525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cultivar) were infected with pathogen (isolate FRM42] of Colletotrichum graminicola, which is a sorghum isolate). RNA was prepared from infected leaves harvested from 45 seedlings 48 hours after inoculation. Note: young seedlings (2 weeks old) exhibit juvenile resistant reaction, which is an incompatible interaction. As they grow older (4 weeks or older), plants resume susceptiblity to anthracmose disease. The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision. WARNING: While most or all ESTs are expected to derive from the host
                                                Location/Qualifiers
1. .532
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/organism="Sorghum bicolor"
/db_xref="taxon:4558"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plant, no effort was made to eliminate ESTs deriving from
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/note="Organ: Anthracnose-infected leaves from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism-"Sorghum bicolor"
/db_xref="taxon:4558"
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Pred. No. 4.3e+02;
""" antches 37;
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                                                                                                                                                                              to exclude PolyA, vector and regions threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                               pathogen-induced plants
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/clone_lib="Pathogen induced 1 (PI1)"
/note="Organ: Anthracnose-infected leaves from
two-week-old sorghum plants 48 hr after inoculation;
Vector: pBluescript II from Lambda Zap II; Site_1: XhoI;
Site_2: EcoRI; Two-week-old sorghum plants (BTX 623
cultivar) were infected with pathogen (isolate FRM42I of
Colletotrichum graminicola, which is a sorghum isolate).
RNA was prepared from infected leaves harvested from 45
seedlings (2 weeks old) exhibit juvenile resistant
reaction, which is an incompatible interaction. As they
grow older (4 weeks or older), plants resume susceptibity
to anthracnose disease. The library was made from poly-A
RNA in the cloning vector lambda ZAP II. Clones to be
sequenced were prepared by mass excision. WARNING: While
most or all ESTs are expected to derive from the host
plant, no effort was made to eliminate ESTs deriving from
the pathogen."

BASE COUNT

96 a 175 c 145 g 116 t
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Query Match 31.5%; Score 31.8; DB 10; Length 532;
Best Local Similarity 59.3%; Pred. No. 4.4e+02;
Matches 54; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
Matches 54; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

Qy 71 ctcctggagcctggtgccctagaagcccacg 101

Db 43 GGAGAAGATGCTGGTGTCCGCCCATGCCCATG 13

Search completed: October 3, 2002, 16:14:49 Job time: 16944 sec

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Title:
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Maximum DB seq length: 2000000000
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score a
and is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
          No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2,

2: /cgn2_6/ptodata/2,

3: /cgn2_6/ptodata/2,

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5: /cgn2_6/ptodata/2,

6: /cgn2_6/ptodata/2,
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Match Length
        Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
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1 US-08-58-136-2
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3 US-08-658-136-2
1 US-08-21-417-2
2 US-08-928-694-9
5 PCT-US91-06950-9
4 US-09-211-417-2
3 US-08-996-083-2
4 US-09-211-417-2
2 US-08-996-083-2
2 US-08-996-65A-140
5 PCT-US95-10398-140
2 US-08-756-506-5
2 US-08-790-65A-139
5 PCT-US95-10398-139
4 US-08-836-075A-17
5 US-08-998-416-580
3 US-08-998-1144
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(c) 1993 - 2000 Compugen Ltd
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137.241 Million cell updates/sec
Sequence 8, Appli
Sequence 3, Appli
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Sequence 18, Appli
Sequence 18, Appli
Sequence 11, Appli
Sequence 1144, App
Sequence 1144, App
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Query Match Best Local S Matches 44

Similarity

27.5%;

Score 27.8; I Pred. No. 10; 0; Mismatches

DB 1;

Length 722;

0;

Gaps

9

Conservative

CLASSIFICATION CLASSIFICATION ATTORNEY/AGENT NAME: Brown, REGISTRATION TELECOMMUNICATION TELEFAX: (61) TELEFAX: (61) INFORMATION FOR SI SEQUENCE CHARACT LENGTH: 722 t LENGTH: 722 TAPE: nucleat STRANDEDNESS: TOPOLOGY: 11t MOLECULE TYPE:	RESULT 1 US-08-702-344-8 US-08-702-344-8 Sequence 8, Application Patent No. 5723315 GENERAL INFORMATION: APPLICANT: Jacobs, APPLICANT: LaVallii APPLICANT: Racle, I APPLICANT: Merberg APPLICANT: Treacy, APPLICANT: Spauldii TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES CORRESPONDENCE ADDRIVENCES CORRESPONDENCE ADDRIVENCES CONFORTE: Massachuse COMPUTER READABLE FO COMPUTER READABLE FO COMPUTER: IBM PCC COMPUTER: IBM PCC COMPUTER: IBM PCC COMPUTER: Patentl CURRENT APPLICATION NUMBER SOFTWARE: Patent CURRENT APPLICATION NUMBER FILLING DATE:	25.6 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5 27.5
CLASSIFICATION: 536 ATTORNEY/AGENT INFORMATION: NAME: Brown, Scott A. REGISTRATION NUMBER: 32,724 TELECOMMUNICATION NIFORMATION: TELEPHONE: (617) 498-8224 TELEPAX: (617) 876-5851 INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear MOLECULE TYPE: cDNA		25.5 3247 4 US-08-718 388-6 25.5 7824 4 US-08-718-388-6 25.5 16382 4 US-08-718-388-8 25.5 16382 4 US-09-128-869-1 25.3 603 4 US-09-422-869-1 25.3 685 2 US-08-451-947-7 25.3 685 2 US-08-424-826A-7 25.3 685 2 US-08-928-694-7 25.3 11958 4 US-09-1134-246-8 25.3 4403765 4 US-09-1134-246-8 25.3 4411529 4 US-09-1134-246-8 25.1 1960 2 US-08-533-306A-1 25.1 1960 2 US-08-533-306A-1 25.1 2680 2 US-08-742-923A-1 25.1 2680 2 US-08-742-923A-1 25.1 2680 2 US-08-533-306A-3
	EOTIDES	Sequence 4. Appl Sequence 6. Appl Sequence 8. Appl Sequence 1. Appl Sequence 7. Appl Sequence 7. Appl Sequence 7. Appl Sequence 7. Appl Sequence 8. Appl Sequence 8. Appl Sequence 1. Appl Sequence 1. Appl Sequence 1. Appl Sequence 1. Appl Sequence 1. Appl Sequence 3. Appl Sequence 3. Appl Sequence 5. Appl

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: LENGTH: 6822
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-426-998-3
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; OTHER INFORMATION: H37Rv
US-09-103-840A-1
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Query Match
Best Local Similarity
                                                                                                                                       SOFTWARE: PATENTIN VER. 2.0 SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/09426998 Patent No. 6358706
                                                                                                                                                                                                                             APPLICANT: DUBIN, ADRIENNE E.
APPLICANT: PYATI, JAYASHREE
APPLICANT: ZHU, JESSICA Y
APPLICANT: ERLANDER, MARK G
APPLICANT: GALINDO, JOSE E
TITLE OF INVENTION: CHANNEL (ALPHAIG T-TYPE CALCIUM
TITLE OF INVENTION: CHANNEL (ALPHAIG-C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local Similarity
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APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007,00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Palentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09103840A Patent No. 6294328
                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/426,998
CURRENT FILING DATE: 1999-10-26
NUMBER OF SEQ ID NOS: 5
                                                                                                                                                                                                                  FILE REFERENCE: ORT-1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11849 aggccccaccgtgtgacgaccggcctcaggagcgcggttgcacctcgacgctcggtggtc 11908
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.5%;
 27.3%;
56.7%;
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 Score 27.6;
Pred. No. 14;
              DB 4;
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              Length 6822;
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US-08-323-443B-1
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; ORGANISM: HOMO SAPIENS
US-09-426-998-4
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                                                                                                                                           APPLICANT: KLINGER, KATHERINE W.
APPLICANT: BURN, TIMOTHY C.
APPLICANT: BURN, TIMOTHY D.
APPLICANT: CONNORS, TIMOTHY D.
APPLICANT: CONNORS, TIMOTHY D.
APPLICANT: GERMINO, GREGORY
APPLICANT: GERMINO, GREGORY
APPLICANT: QIAN, FENG
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: Darby 6 Darby PC
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Applicati
Patent No. 5654170
GENERAL INFORMATION:
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LENGTH: 7741
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/426,998
CURRENT FILING DATE: 1999-10-26
NUMBER OF SEQ ID NOS: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: ERLANDER, MARK G
APPLICANT: GALINDO, JOSE E
TITLE OF INVENTION: DAN ENCODING HUMAN ALPHAIG T-TYPE CALCIUM
TITLE OF INVENTION: CHANNEL (ALPHAIG-C)
FILE REFERENCE: ORT-1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PATENTIN VER. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5941 gagtecacetgetacaacacggtcateteg 5970
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                                                                                                             CITY: New York
STATE: NY
                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 ggggagtcctcctggagcctggtgccctag 92
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                                                                                                                                                                                                                                                                                                                                                                                                      Application US/08323443B
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                                                                                              USA
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Pred. No. 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-658-136-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 6071717
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 31571 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16488 TGAGGCCTCCGGGTCCTGGG 16507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL: NO ORIGINAL SOURCE: ORGANISM: Home
   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,8
                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTED:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: GENZYME C
                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                             APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                             COUNTRY:
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REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION:
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                                                                                                                                                                                                                            FRAMINGHAM
                                                                                                                                                                                                            MASSACHUSETTS
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GERMINO, GREGORY
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ELIZABETH
UMBER: 31,845
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58.8%;
                                                                                                                                                                                                                                                                                     POLYCYSTIC KIDNEY DISEASE GENE
58
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                                                                                                      Release #1.0, Version #1.25
                                                                           us/08/658,136
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Pred. No. 22;
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STRANDEDNESS:
TOPOLOGY: lir
MOLECULE TYPE:
US-08-658-136-1
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Best Local :
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                                                                                       TELEFAX: 508-872-5415
INFORMATION FOR SEQ ID NO: 1:
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,845
REFERENCE/DOCKET NUMBER: GEI
                                                SEQUENCE CHARACTERISTICS:
LENGTH: 53577 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: QIAN, FENG
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
NUMBER OF SEQUENCES: 58
                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                    TELECOMMUNICATION INFORMATION:
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LENGTH: 53526 base pairs
TYPE: nucleic acid
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                                                                                           TELEPHONE: 500-872-5415
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                                                                                                                                                                                                                                   APPLICATION NUMBER:
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STATE: MASSACHUSETTS
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47; Conserv
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LANDES, GREGORY
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                          linear
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             DNA (genomic)
                                      single
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Pred. No. 23;
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US-08-451-947-9/c
Sequence 9, Application US/08451947
Patent No. 5702906
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              Query Match
Best Local Similarity 5/...
Thes 49; Conservative
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Best Local Similarity
Matches 47; Conservai
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: 07/648482
FILING DATE: 31-JAN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/587707
FILING DATE: 1991
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PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/426419
FILING DATE: 19-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,947
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MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
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APPLICATION NUMBER:
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APPLICANT: ROSENTHAL, ARNON
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TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                                 NAME: Torchia, Timothy E. REGISTRATION NUMBER: 36,700 REFERENCE/DOCKET NUMBER: 66
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                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
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                                                                                                                              linear
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                                                 26.5%;
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58.8%;
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                                   Score 26.8; DE Pred. No. 20; 0; Mismatches
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Pred. No. 23;
0; Mismatches
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                                 Indels
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RESULT 10
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Best Local Similarity 57.0%;
Matches 49; Conservative
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/587707
FILING DATE: 25-5EP-1990
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: 08/240387
FILING DATE: 10-May-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 415/225-8674
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                                                                                                                               469 TGTCGAGGATGGGGTTAGGACTCCAATGACACACTGGGGAGGAGGAAAATGAGGGGGATG 410
                                                                   409 CGGAGGGAGCCTGGGGGAGCAGGAGC 384
                                                                                     71 ctcctggagcctggtgccctagaagc 96
                                                                                                                                                    409 CGGAGGGAGCCTGGGGGAGCAGGAGC 384
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TYPE: Nucleic Acid
STRANDEDNESS: Sing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Torchia, PhD., Timoth
REGISTRATION NUMBER: 36,700
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                                                                                                                                                                                                   Score 26.8; D
Pred. No. 20;
0; Mismatches
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RESULT 11
PCT-US91.06950-9/c
Sequence 9, Application PC/TUS9106950
GENERAL INFORMATION:
GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
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                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: PO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 31-JAN PRIOR APPLICATION DATA:
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APPLICATION NUMBER: 08/451947
FILING DATE: 26-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44
CUMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 22-MAR-1993
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                 71 ctcctggagcctggtgccctagaagc 96
                                                                                                                                                                                                                                                                                                                                                                    TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Torchia, PhD., Timothy E. REGISTRATION NUMBER: 36,700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/426419 FILING DATE: 19-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
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            GENENTECH, INC. ROSENTHAL, ARNON
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NOVEL NEUROTROPHIC FACTOR
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Pred. No. 20;
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Best Local Similarity
Watches 49; Conserve
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                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: RAILDEY, Jerome B
APPLICANT: Whitehead, Clark M
TITLE OF INVENTION: NUCLEOLUS AUTOANTIGENIC MARKER FOR SYSTEMIC LUPUS
TITLE OF INVENTION: ERHYEMATOSUS
TITLE OF INVENTION: Genbank
TITLE OF INVENTION: Accession Number U86751
                                                                NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver.
SEQ ID NO 2
LENGTH: 3286
                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09211417A Patent No. 6177254
                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/211,417A CURRENT FILING DATE: 1998-12-15
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
OTHER INFORMATION: Nucleic Acid Sequence of ASE-1
                 FEATURE:
                              ORGANISM: Homo sapiens
                                                    TYPE: DNA
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LENGTH: 1190 bases
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REFERENCE/DOCKET NUMBER: 661
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/266-1994
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PRIOR APPLICATION NUMBER: 07/648482
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CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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CITY: South San Francisco
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57.0%;
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Pred. No. 20;
0; Mismatches
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APPLICANT: Magna, Holly
APPLICANT: Schaffer, Paul
APPLICANT: Schaffer, Paul
APPLICANT: Schaffer, Paul
APPLICANT: Yocum, Michael
APPLICANT: Mitchaell, Peter
APPLICANT: Mitchaell, Peter
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: HUMAN NUCLEOTIDE PYROPHOSPHOHYDROLASE-2
FILE REFERENCE: PF-0420 US:
CURRENT APPLICATION NUMBER: US/08/996,083A
CURRENT FILING DATE: 1997-12-22
NUMBER OF SED ID NOS: 3
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US-09-429-516-2
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                                                                                       GENERAL INFORMATION:
APPLICANT: Magna, H
APPLICANT: Schaffer
APPLICANT: Lawton,
APPLICANT: Yocum, S
APPLICANT: Mitchell
APPLICANT: Hutchins
APPLICANT: Murry, I
                                                                                                                                                                                                                 Sequence 2, Application US/09429516 Patent No. 6251389
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Best Local Similarity 57.0
Matches 49; Conservative
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Best Local Similarity
Matches 37; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
OTHER INFORMATION: Incyte Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                             CORRESPONDENCE ADDRESS
                                                       APPLICANT: HUTCHINSON, NANCY
APPLICANT: MUTTY, LYNN E.
TITLE OF INVENTION: HUMAN NUCLEOTIDE PYROPHOS
TITLE OF INVENTION: PHOHYDROLASE-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH: 4183
                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                         636 gtgtccagggtgcagccttgacacct 661
                                                                                                                                                                                                                                                                                                                                                               840 GGATCCTTAGGGTGCCCTGGGGGGCTGAGGCACAGGTGAGTCCACCTCCTGCCT 787
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3174 Porter Drive
                                                                                                                      Mitchell, Peter
                                                                                                                                                                  Schaffer, Paul
                                                                                                                                     Yocum, Sue
                                                                                                                                                                                    Magna, Holly
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              Incyte Pharmaceuticals, Inc.
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57.0%;
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Pred. No. 23;
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US-08-290-665A-140/c
; Sequence 140, Application US/08290665A
; Patent No. 5882852
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Best Local :
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                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
2IP: 10154
COMPUTER READBLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN &
                                                                                                                                                                                                                                                               APPLICANT: BUKH, J., APPLICANT: PURCELL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
LIBRARY: SATPF
CLONE: 1388013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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LENGTH: 4183 base pairs
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MEDIUM TYPE: Diskette
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                                                                                              STREET: 345 PARK AVENUE CITY: NEW YORK STATE: NEW YORK
                                                                               COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
CORE GENES OF ISOLATES OF HEPATITIS C VIRUE
AND THE USE OF REAGENTS DERIVED FROM THESE
SEQUENCES IN DIAGNOSTIC METHODS AND VACCINE
263
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Pred. No. 23;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,665A
FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 2026-4116
TELECOMMUNICATION INFORMATION:
"TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEFAX: (212) 751-6849
TELEFAX: (212) 751-6849
TELEFAX: 1212) 751-6849
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Search completed: October 3, 2002, 16:21:45 Job time: 16945 sec
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Hest Local Similarity 56.2%; Pred. No. 21;
Matches 50; Conservative 0; Mismatches
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Maximum DB :
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Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compugen Ltd
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23.9	68.9 27.2	71.2 69.2	87.9	100.0	Query Match Length DB	œ
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22 21	22 22	22 22	22	22	BB	
AAH43682 AAC98774	AAD03295 ABA08485	AAD03321 AAD03319	AAD03320 AAD03296		ID	SUMMARIES
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AAL18884	AAF08150	AAL10935	AAI08354	AAI47988	AAI22692	AAK41922	AAK16181	ABA34826	ABA67769	ABA49850	AAA51352	AAK73303	ABI99496	AAI03344	AAI34821	AAI13465	AAK28874	AAK03423	ABA24907	ABA55162	ABA44706	AAC01661	ABL18856	AAS84267	AAH43683	AAH35203	AAH07561	AAS84265	AAK72741	AAK72740	AAH43684	ABL18857	AAH14839	AAX06882	AAT85927
Human breast cance	-	breast canc	#8345 u	#16674 used		bone n	æ		Human foetal liver	Human breast cell	D)		ischaemic c	#3335 used	#3507	#3398	bone n	brain	#3373 f	foetal		Human secreted pro	Drosophila melanog	DNA encoding novel	PRKAG3 intron 4 -		Human cDNA clone	_			PRKAG3 intron 10	Drosophila melanog	Human cDNA sequenc	Disease associated	Mammalian AMPK-gam

ALIGNMENTS

Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant; metabolic disease; diabetes; obesity; substitution; ss.

Homo sapiens

PRKAG3 CDNA. 21-JAN-2002

(first entry)

RESULT AAH43685

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AAH43685 standard; cDNA; 1647

BP.

AAH43685;

variation CDS variation variation /*tag= b /1abel= "C230G" /note= "Causes P71A" /"rag" C /label= "T559C" /note= "Silent variation" 1037 /product= "PRKAG3" 230 /*tag= d /label= "C1037T" /note= "Causes R340W" Location/Qualifiers 20..1489

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Matches
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           421
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(AMP) activated kinase (AMPK) gamma subunit muscle-specific isoform, complete PRKAG3. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders suc as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3.
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ttcctagagcaagaaaacagcagctcatggccatcaccagctgtgaccagcagctcagaa

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cc useful as therapeutic for treating carbohydrate metabolism disorders such cas diabetes, obesity, and disorders associated with muscle metabolism cs such as myopathy and cardiovascular diseases, to modulate AMPK cc activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic cevaluation, genetic testing and prognosis of a metabolic disorder. Cc evaluation, genetic testing and prognosis of a metabolic disorder. Cc evaluation of carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are cc useful for detecting a dysfunction of carbohydrate metabolism resulting cf rom the expression of a functionally altered allele of PRKAG3.

Cc Transgenic animal and host cell transformed with PRKAG3 or a creening compounds able to modulate AMPK activity. Nucleic acid cencoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or of pRKAG3 is useful for detecting mutations beta synthase (CBS) domain of pRKAG3 is asseful to constant cystathione beta synthase (CBS) domain or of pRKAG3 is asseful to constant cystathione beta synthase (CBS) domain or of pRKAG3 is asseful to constant cystathione beta synthase (CBS) domain or of pRKAG3 and is asseful to constant cystathione beta synthase (CBS) domain or of pRKAG3 and is asseful to constant cystathione beta synthase (CBS) domain or of pRKAG3 and is asseful to constant cystathione beta synthase (CBS) domain or of pRKAG3 and is asseful to constant cystathione beta synthase (CBS) domain or of pRKAG3 and the constant cystathione beta synthase (CBS) domain or of pRKAG3 and the constant cystathione beta synthase (CBS) domain or of pRKAG3 and the constant cystathione beta synthase (CBS) domain or of pRKAG3 and the constant cystathione beta synthase (CBS) domain or of pRKAG3 and the constant cystathione beta synthase (CBS) domain or of pRKAG3 and the constant cystathione constant cystathione constant cystathione constant cystathione constant 
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The present sequence is pig adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3 splice variant DNA. Prkag3 gene is located in the RN locus of chromosome 15. Mutation in prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, Claim 12; Page 69; 71pp; English

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                                                                                                                                                                                                                   CC (AMP) activated kinase (AMPX) gamma subunit muscle-specific isoform, CC complete PRRAG3. Prkag3 gene is located in the RN locus of chromosome CC 15. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRRAG3 is useful as CC therapeutic for treating carbohydrate metabolism disorders such as CC diabetes, obesity, and disorders associated with muscle metabolism CC such as myopathy and cardiovascular diseases, to modulate AMPX CC activity, and for restoring a normal AMPX function. PRRAG3 sequence CC and its functionally altered mutants are useful for the diagnostic cevaluation, genetic testing and prognosis of a metabolic disorder, CC preferably a carbohydrate metabolism disorder. Primers that can detect ca genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting CC from the expression of a functionally altered allele of PRKAG3. CC heterotrimeric AMPX consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPX activity. Nucleic acid cencoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain cc of PRKAG3 and is useful in gene therapy.
                                                                                                                                            Query Match
Best Local Similarity
Matches 1315; Conser
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                    Claim
                                                                        New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of associated with energy metabolism such as diabetes, obesity,
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CC (AMP) -activated kinase (AMPK) gamma subunit muscle-specific isoform, CC PRKAG3. Prkag3 gene is located in the RN locus of chromosome 15.

CC Mutation in Prkag3 results in an altered regulation of carbohydrate CC metabolism, particularly in skeletal muscle. PRKAG3 is useful as CC therapeutic for treating carbohydrate metabolism disorders such as CC diabetes, obbsity, and disorders associated with muscle metabolism CC such as myopathy and cardiovascular diseases, to modulate AMPK CC activity, and for restoring a normal AMPK function. PRKAG3 sequence CC and its functionally altered mutants are useful for the diagnostic CC valuation, genetic testing and prognosis of a metabolic disorder. CC preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are CC useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3. CC Transgenic animal and host cell transformed with PRKAG3 or a carbohydrate animal and host cell transformed with PRKAG3 or a carbohydrate animal and host cell transformed with PRKAG3 or a carbohydrate animal and host cell transformed with PRKAG3 or a carbohydrate animal and host cell transformed with PRKAG3 or a carbohydrate animal and sequence encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain CC of PRKAG3 and is useful in gene therapy.

日 δ Бp Ŷ В Ş

Sequence 1867 BP; 380 A; 583 C; 529 G; 375 T; 0 other;

68.9%; 85.7%;

DB

22;

Length

1867;

δÃ 밁 Ş Q В 밁 Ş Q В 밁 Ş 밁 Š 망 δÃ 밁 γ 밁 Š 밁 δ Query Match
Best Local Similarity
Matches 1309; Conserv 598 869 538 638 478 578 418 518 361 458 301 398 338 101 241 281 121 221 161 181 61 gcacctttgtgggacagcaagaagcagagcttcgtggggatgctgaccatcacagacttc gacaccatgctggagatcaagaaggccttctttgccctggtggccaacggcgtccgagcg gacaccatgctggagatcaagaaggccttctttgctctggtggccaacggtgtgcgggca ttcatgcaggagcacacctgctacgatgccatggcaactagctccaagctagtcatcttc tttcccaagctgggctgggatgacgaactgcggaaacccggcgcccagatctacatgcgc tgtgagctagaaggcctgcagaagaggcctgccctgtgcctgtccccgcaggcccca ggctccagcacagatgatgtggagctggccacggagttcccagccacagaggcctgggag agaatccgtgggaaacggagggccaaagccttgagatggacaaggcagaagtcggtggag ttcatgcaggagcacacctgctacgatgccatggcgaccagctccaaactggtcatcttc ttacccaggctgggctgggatgatgagctgcagaagccgggggcccaggtctacatgcac gatgagct----tgggctggtggaagagaagccagcccgtgcccatccccagaggtgctg gactccaacacagaccatctggatctgggcatagagttctcagcctcggcggcgtcgggg gtggacaaccccccaacagagcgggacatcctcccctctgactgtgcagcctcagcctcc 9t999cactccaccaacagggtgggactgcctcccctctgactgtacagcctcagctgca gggcaggaggccacattccccaaggccacacccttggcccaagccgctcccttggccgag 999ct99a99ccacattccccaaa9accacacccttggctcaagctgatcc---tgccggg gaagggggcctccggggcccgagggaaggtccccagtccaggccagttgctgagtccacc gaaggggagccaccaggtcagggggaaggtccccggtccaggccagctgctgagtccacc agaagccatggggaccaggggaacaaggcctctagatggacaaggcaggaggatgtagag ttcctagagcaaggagagccgttcatggccatcccgagctgtaaccaccagctcagaa Conservative 0 Score 1134.4; | Pred. No. 4.1e-: 0; Mismatches Indels .. Gaps 577 657 697 537 637 417 517 457 397 180 120 477 360 300 240 337 60 4.

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 haematopoiesis regulation;
                                               Human AMP-activated protein kinase subunit homologue cDNA,
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proliferation; metastasis; cancer; tumour; haematopoietic disord myeloid cell disorder; lymphoid cell disorder; asthma; arthritis chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerolic; cytostatic; inhibin; chemotaxis; chemokinesis; vulnerary; antiulcer; osteopathic; vasotropic; cardiant; virucide; antibacterial; thrombolysis; oncogenesis; haematopoietic disorder; arthritis;

WO200157188-A2

09-AUG-2001

05-FEB-2001; 2001WO-US03800

03-FEB-2000; 27-APR-2000; 2000US-0496914 2000US-0560875

(HYSE-) HYSEQ INC

Tang Liu Ċ, Drmanac

2001-457740/49 DB; ABB11241.

Claim 1; Page 429; 1963pp; English

Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and CS sequences ABA08235-ABA09574 represent nucleic acids encoding them. The CS invention also relates to vectors and recombinant host cells comprising a CC nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which CC bind to polypeptides of the invention. Although novel, many of the CC polypeptides of the invention have homology to known proteins, thereby CC giving an insight into their probable biological activities, and hence CC potential therapeutic applications. The polypeptides of the invention may that we various activities; stem cell growth factor activity; climmunomodulatory activity; stem cell growth activity; immunomodulatory activity; stem cell growth activities; chemotactic or chemokinetic activities; haemostatic, thrombotic or thrombotic or chemokinetic activities; haemostatic, thrombotic or thrombotic or chemokinetic activities; haemostatic, thrombotic or conditions, e.g., by protein or gene therapy. Such conditions include cancer cell proliferation or metastasis.

CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis), protein or gene therapy. Such conditions include cancer cell proliferation or arthritis), bene disorders (e.g., myeloid or lymphoid cell carcerial ischaemia, bone disorders (e.g., myeloid or lymphoid cell carcerial ischaemia, bone disorders (e.g., osteoporosis), and abnormal cepair (or nucleic acids encoding them) may be used to promote wound bacterial and fungal infections in addition to immune disorders to conterides with growth factor activity may be used in cell cultures to Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a cDNA encoding a novel human polypeptide of the invention.

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metabolic disease; diabetes;
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946..989
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obesity; substitution; ds.
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequences given in AAH43681-84 represents genomic encoding the human AMP-activated protein kinase gamma (PRKAG3). Detecting the presence of the PRKAG3 DNA, or is useful in determining a risk estimate of a metaboli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and for determining a risk estimate of diseases in subject by detecti
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AAC98774

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Matches 580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid that is a pancreatic cancer antigen for preventing, treating, or ameliorating a medical condition, particular pancreatic cancer, or for use in assays for diagnosing a pathological condition
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated 5'-AMP-activated protein kinase subunit(s) - us develop products for treating e.g. hyper-cholesterolaemia, o hypoxia, ischaemia, nutrition disorders or diabetes mellitus
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                                                     Bandman
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                                                                                                                                                                                                                                                                                                                                                                                                              multiple sclerosis; myasthenia gravis; osteoarthritis; osteoporosis; pancreatitis; polycystic kidney disease; polymyositis; scleroderma; Sjorgren's syndrome; autoimmune thyroiditis; cancer; infection; trauma;
WPI; 1999-080952/07
                                                                                           (INCY-) INCYTE PHARM INC
                                                                                                                                                                    19-JUN-1998;
                                                                                                                                                                                                          23-DEC-1998.
                                                                                                                                                                                                                                              W09858052-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          atopic dermatitis; dermatomyositis; diabetes mellitus;
glomerulonephritis; gout; Grave's disease; lupus erythematosus;
                                                                                                                               19-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Matches 567
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27-AUG-1999;
11-JAN-2000;
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         Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection
                                                               Ota T,
Ishii :
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                                                                                                                                                                                                                                                                                                    Human cDNA sequence
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                                                                                                                                                                                                                                                                                                                                                                    AAH14839 standard; cDNA;
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2000JP-0183767.
2000JP-0241899.
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99JP-0300253
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T, Wakama
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Nagai K,
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to the complementary strand of a polynucleotide which comprises one of CC the 5602 nucleotide sequences defined in the specification, where the CC ollgonucleotide comprises at least 15 nucleotides; or (b) a combination CC of an oligonucleotide comprising a sequence complementary to the CC complementary strand of a polynucleotide which comprises a 5'-end cC sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence complementary to a CC polynucleotide which comprises a 1 least 15 nucleotides and the combination of the 5'-end sequence, '-end sequence, where the CC the 5'-end sequence, '-end sequence, where the CC the 5'-end sequence, '-end sequence, where the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, CC the specification and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs and Sequences; AAH3632 to AAH3632 to AAH3632 to AAH3632 and CAAH3633 to AAH3742 represent human cold sequences; AAB9246 to AAH3633 control of the present oligonucleotides, all of which are used in the exemplification of the present invention.
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                                                                             The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from prosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176 ABLIG171), expressed DNA sequences (ABLIG175) and the encoded proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gatgccatggcaactagctccaagctagtcatcttcgacacccatgctggagatcaagaag
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539; Conserv
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                      1461
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; Pred. No. 6.1e
0; Mismatches
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6.1e-68;
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RESULT
AAH43684
                The sequences given in AAH43681-84 represents genomic fragments encoding the human AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution P71A; in exon 4 variation may be a substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a Substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution R340W. There may also be nucleotide variatin in intron 6.
                                                                                                                                                                                     New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and edetermining a risk estimate of diseases in subject by detecti
                                                                                                                                                          Example 1;
                                                                                                                                                                                                                                                      Andersson
                                                                                                                                                                                                                                                                           (AREX-) AREXIS
                                                                                                                                                                                                                                                                                               07-APR-2000;
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857..1014
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740..856
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42..79
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obesity; substitution;
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                           the
variation
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Sequence

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BP;

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271

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Best Local Similarity 97.6%;
Matches 283; Conservative
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AAK72740
      04-FEB-2000
24-FEB-2000
02-MAR-2000
11-MAR-2000
11-MAR-2000
19-MAY-2000
07-JUN-2000
28-JUN-2000
30-JUN-2000
07-JUL-2000
11-JUL-2000
11-AUG-2000
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                                                                                                                                                                                                                                                                                                            31-JAN-2000;
                                                                                                                                                                                                                                                                                                                                    17-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                   W0200157182-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                 cytostatic; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                               Human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immune/haematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                              immune;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
     2000US-0179065.
2000US-0184664.
2000US-0186350.
2000US-0189874.
2000US-0198123.
2000US-0294515.
2000US-0214886.
2000US-0214886.
2000US-0216887.
2000US-0218290.
2000US-0218290.
2000US-0228318.
2000US-0228318.
2000US-0228314.
2000US-0228326.
2000US-0228326.
                                                                                                                                                                                                                                                                                                                                  2001WO-US01354
                                                                                                                                                                                                                                                                                                                                                                                                                             haematopoietic; immune/haematopoietic antigen; cancer; ne therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antigen genomic sequence SEQ ID NO:27552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 278.8; DB 22;
Pred. No. 8.3e-63;
0; Mismatches 7;
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  14 - AUG - 2000
11 - AUG - 2000
12 - AUG - 2000
22 - AUG - 2000
23 - AUG - 2000
23 - AUG - 2000
20 - SEP - 2000
01 - SEP - 2000
01 - SEP - 2000
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2000US-0227182
2000US-0229343
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2000US-0239343
2000US-02311414
2000US-0231401
2000US-0231401
2000US-0231417
2000US-0231417
2000US-0231417
2000US-0231417
2000US-02317034
2000US-02346476
2000US-02346476
2000US-02346476
2000US-02346525
2000US-02346525
2000US-02346526
2000US-02346526
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ARS4951 to AAK64702 encode the human immune/haematopoietic antigen (1) CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic c activity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased cytostated with eactivity of (I) by expressions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to CC supplement the patients own production of (I). Additionally, (I) CC polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the CC protein. (I) proteins and polynucleotides may be used to prevent, CC diagnose and treat immune/haematopoietic-related diseases, especially concers and cancer metastases of haematopoietic antigen genomic conservation the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-NOV-2000
11-NOV-2000
01-DEC-2000
01-DEC-2000
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17 NOV - 2000
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17-NOV-2000;
17-NOV-2000;
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                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 27552; 3071pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                  metastasis -
                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding
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2000US-0249215
2000US-0249216
2000US-0249217
2000US-0249245
2000US-0249245
2000US-0249264
2000US-0249265
2000US-0249267
2000US-0249267
2000US-0249267
2000US-0249299
2000US-0259391
2000US-0259391
2000US-0251868
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2000US-0249211.
2000US-0249211.
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2000US-0249213
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2000US-0249208
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2000US-0246532
                                                                                                                                                                                                                                                                                                                                                                                                      SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                   SCI INC
                                                                                                                                                                                                                                                                                                                           human immune/hematopoietic antigen polypeptides, diagnosing and/or treating cancers and
                                                                                                                                                                                                                                                                                                                                                                                                      Ruben
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Query Match

15.3%;

Score

252;

DB

22;

Length 3425

Sequence

3425

BP;

916 A;

794 ე:

951 G;

764

, ;

0 other;

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Best Local Similarity Matches 252; Conser
3185
            1636
                          3245
                                       1576
                                                    3305
                                                                              3365
                                                                                           1456
                                                                                                         3425
                                                                                                                      1396
                                                                 1516
                                                 ctcttagtcttc
                       CCCCCATTIGCTGGTTCAGCTATGATTCAGGTAGGCTCTGCCCTGGGCCATGACACCAGC
                                                                            CTCTTAGTCTTC
                                                                                                                                   ilarity 100.0%;
Conservative
            1647
3174
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ALIGNMENTS

REFERENCE AUTHORS VERSION KEYWORDS SOURCE DEFINITION ACCESSION RESULT BI344527 FEATURES COMMENT LOCUS JOURNAL TITLE ORGANISM source Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Tex: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore FORWARD: AGGAAACAGCTATGACCAT BACKWARD: GTTTTCCCAGTCAGCACG Plate: 119 row: I column: 11 Seg primer: ATTTAGGTGACACTATAG. BI344527 572 bp mRNA linear 373008 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence. BI344527 BI344527.1 GI:15037807 EST. and -minmatch 12 options. PCR PRimers Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine Unpublished (2000) and Keele, J.W. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 572)
Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegre Sus scrofa /organism="Sus scrofa" /db_xref="taxon:9823" /clone_lib="MARC 2PIG" /tissue_type="pooled" /lab_host="DH10B" Location/Qualifiers /note="Vector: PCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Bennett, G.A., Laegreid, W.W. Euteleostomi; Sus. EST 30-JUL-2001 18

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AUTHORS
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Li, W.B., Gruber, C., Jessee, J. and Polayes, Full-length cDNA libraries and normalizati Unpublished (2001) Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.Location/Qualifiers
                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 970)
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prime, mRNA sequence.
AL533446
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       www.genoscope.cns.fr
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/tissue_type="Adult brain"
/note="Vector: pcMySpORT 6; Site_1: Not1; 1st strand cDNA
/note="Vector: pcMySpORT 6; Site_1: Not1; 1st strand cDNA
was primed with a Not1-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcMySpORT 6
vector. Library was constructed by Life Technologies.
Contact : Feng Liang Life Technologies, a division of
Invitrogen 9800 Medical Center Drive Rockville, Maryland
20850, USA Fax: (1) 301 610 8371 Email:
filang@lifetech.com uRL:
http://fulllength.invitrogen.com"

55 a 230 c 217 g 268 t
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/db_xref="taxon:9606"
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Pred. No. 6.8e-80;
D; Mismatches 310;
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MEDLINE
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Best Local Similarity
Matches 518; Conserv
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                                 GACTCCTTTAAGCCGTTGGTCTGCATCTCCCCCAATGCCAGCCTTTTTGATGCCGTCTCC
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Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html
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Cellular Immunology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Abdrakhmanov.l., Lodygin,D., Geroth,P.,
,J., Korn,B. and Buerstedde,J.M.
A large database of chicken bursal ESTs
analysis of vertebrate gene function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
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                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Gallus gallus"
/strain="CB"
/db_xref="taxon:9031"
/clone="25f16r1"
/clone_lib="dkfz426"
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238 c 186 g 166 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                       Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., It,
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matguu
                                         Watahiki,M., Yoneda,Y., Isl
,S., Kawai,J., Okazaki,Y.,
                                                                                                                                                                                                                                                                                                          Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishi,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
                                                                                                                                                                                                                                                                                                                                                                                                                         RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 685 bp mRNA linear
BB630381 RTKEN full-length enriched, 6 days neonate
musculus cDNA clone A030014A04 5', mRNA sequence.
BB630381
                           Hayashizaki,Y.
                                                                                                                                                                                                                                                                     Tel: 81-45-503-9222 Fax: 81-45-503-9216
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RIKEN integrated sequence analysis (RISA) system -- 384 - format
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Rodentia; Sciurognathi; Muridae; Murinae;
                                         hikawa,T., Ozawa,K., Tanaka,T., Matsuura
Muramatsu,M., Inoue,Y., Kira,A. and
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awa 230–0045, Japan
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                                                                                                                                                                                                                                CACAGTGGGGGTCCAGAGAGTCAAGAGATGGACTTCTTAGAACAAGGAGA---AAACTCA 117
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Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,
,Y. and Hayashizaki,Y.
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further details.
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/dev_stage="6 days neonate"
/lab_host="DH10B"
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/clone_lib="RIKEN full-length enriched,
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/db_xref="taxon:10090"
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                                                                                 TGTATACTTCCTTCATGAAGTCTCATCGCTGCTATGACCTGATTCCCACAAGCTCCAAAT 126
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1 (bases 1 to 921)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="LTT_NFL006_PL2"
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/tissue_type="placenta"
/note="wector: pcMvSPORT 6; Site_1: NotI; 1st strand cDNA
/note="wector: pcMvSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco Rv sites of the pcMvSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: fliang@lifetech.com URL:
                                                                                                                                                                                                                                                                                                                                          http://fulllength.invitrogen.com"
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/db_xref="taxon:9606"
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.geno:
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Prime, mRNA sequence.
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/clone="CSD0K007YED2"
/clone="CSD0K007YED2"
/clone="CSD0K007YED2"
/tissue_type="placenta"
/note="vector: pcwVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: flang@lifetech.com URL:
http://fulllength.invitrogen.com"
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       ctctggtctccatctcctaatgatagcctgtttgaagctgtctacaccctcatcaaga
                                                                             agattgaacaacataagattgagacctggagggagatctacctgcaaggctgcttcaagc
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                                                                                                                                                                     tcactgacttcatcctggtgctgcatcgctactactaggtcccccctggtccagatctatg
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                                                                                                                                                                                                                                                                                                                                TGGTTGTATTTGATACGTCCCTGCAGGTGAAGAAGCTTTTTTTGCTTTGGTGACTAACG
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                                                     AGCTAGAAGAACACAAGATAGAAACTTGGAGAGAGGTGTATCTCCAGGACTCCTTTAAAC
                                                                                                                                               TCACTGATTTCATCAATATCCTGCACCGCTACTATAAATCAGCCTTGGTACAGATCTATG
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/note="Yector: pCMVSPORT 6; Site_1: NotI; 1st strand
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/db_xref="taxon:9606"
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467815 MZ
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                                                                                                                                                    Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904 e. Vector identified by cross_match with the -minscore
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Contact: Smith TPL
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                                              BACKWARD: GTTTTCCCAGTCACGACG
Plate: 90 row: I column: 1
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PCR PRimers
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Fax: 402 762 4390
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PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                            FORWARD: AGGAAACAGCTATGACCAT
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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                     primer: ATTTAGGTGACACTATAG
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                                                                    prime, mRNA
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AL552459.1
Eukaryota: Metazoa: Chordata: Mammalla: Eutheria: Primates: 1 (bases 1 to 908)
Li,W.B., Gruber,C., Jessee,J.
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                                       Homo sapiens
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/organism-"Bos taurus"
/db_xref-"taxon:9913"
/clone_lib-"MARC 2BOV"
/tissue_type-"pooled"
/lab_host-"DH10H"
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                                                                     GI:12891378
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and
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Genoscope - Centre National
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Contact: Genoscope
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/clone="Lib="LTI_NFL006_PL2"
/tissue_type="placenta"
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/notice="Vector: pcMVSPORT 6; Site_3: NotI; 1st strand cDNA
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segref@genoscope.cns.fr,
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Conservative 21.3%; Score 350; DB 9; Pred. No. 6.7e-72; 1; Mismatches 266 Mismatches 266; Indels 0 Gaps

tctacatgcgcttcatgcaggagcacacctgctacgatgccatggcaactagctccaagc 626

tcactgacttcatcctggtgctgcatcgctactacaggtcccccctggtccagatctatg GTGTACGAGCTGCCCCTTTATGGGATAGTAAGAAGCAAAGTTTTGTGGGCATGCTGACCA 9t9t9c9g9cagcccctctatg9gacagcaagaagcagagctttgtg9g9atgctgacca tagtcatcttcgacaccatgctggagatcaagaaggccttctttgctctggtggccaacg 686 TGTATACTTCCTTCATGAAGTCTCATCGCTGCTATGACCTGATTCCCACAAGCTCCAAAT 190 806 310 250

agattgaacaacataagattgagacctggagggagatctacctgcaaggctgcttcaagc 866

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accggatccatcgcctgcctgttcttgacccggtgtcaggcaacgtactccacatcctca 550

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603384001F1 NIH_MGC_87 Homo:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D Email: cgapbs-r@mail.nih.gov
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National Institutes of Health, Mammalian
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Plate: LLAM12001 row: a column: 02
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                                                                                                                                                                                                                                                                                                                                                  Conservative
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/db_xref="taxon:9606"
/clone="IMAGE:5392777"
/clone_lib="NIH_MGC_87"
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                                                                                                                                                         Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
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                                                                                                                 segref@genoscope.cns.fr,
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="CSODA012YB06"
/clone_lib="LTI_NFL011_NBC1"
                                                                    /organism="Homo sapiens"
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//tissue_type="neuroblastoma cells"
//tissue_type="neuroblastoma cells"
//lab_nost="DHIOB"
//note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
//note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
//note="Organ: brain; Vector: pcMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library is not normalized, but is the control for
the normalized libraries. Library was constructed by Life
Technologies. Contact: Fing Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
// Maryland 20850, USA Fax: (1) 301 610 8371 Email:
fliang@lifetech.com URL:
http://fulllength.invitrogen.com"
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Contact: Genoscope
Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France BP 191 91006 EVRY cedex - Grance Frueb : www
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AGENCOURT_6427350 NIH_MGC_72
5', mRNA sequence.
BM462694
BM462694.1 GI:18511734
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                         CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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/note="norgan: skin; Vector: pcMV-SPORT6; Site_1: Not1;
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Best Local S
Matches 482
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                      tectetacegeactatecaagatttgggeatcggeacatteegagaettggetgtggtgg 1106
                                                                                     accggatccatcgcctgctgttcttgacccggtgtcaggcaacgtactccacatcctca
                                                                                                                                                                                                                              ctctggtctccatctctcclaatgatagcctgtttgaagctgtctacaccctcatcaaga 926
                                                                                                                                                                                                                                                                                                     agattgaacaacataagattgagacctggaggggagatctacctgcaaggctgcttcaagc
                                                                                                                                                                                                                                                                                                                                                       TCACTGATTTCATCAATATCCTGCACCGCTACTATAAATCAGCCTTGGTACAGATCTATG
                                                                                                                                                                                                                                                                                                                                                                          tcactgacttcatcctggtgctgcatcgctactacaggtcccccctggtccagatctatg 806
                                                                                                                                                                                                                                                                                                                                                                                                                          GTGTACGAGCTGCCCCTTTATGGGATAGTAAGAAGCAAAGTTTTGTGGGCATGCTGACCA
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                                                                  CCCACAAGCGCATTCTGAAGTTCCTCAAATTGTTTATCACTGAGTTCCCCCAAGCCAGAGT
                                                                                                                                         ACAAGATCCACAGGCTGCCAGTTATTGACCCCAGAATCAGGCAATACTTTGTACATCCTCA
                                                                                                                                                                                                              CGCTTGTCTGCATTTCTCCTAATGCCAGCTTGTTTGATGCTGTCTCTTCATTAATTCGGA
                                                                                                                                                                                                                                                                                  AGCTAGAAGAACACAAGATAGAAACTTGGAGAGAGTGTATCTCCAGGACTCCTTTAAAC 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
Contact: Robert Strausberg, Ph.D Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tissue Procurement: Lou Staudt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plate: LLAM12269 row: m column: High quality sequence stop: 745.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       malia; Eutheria; Primates; Catarrhini;
(bases 1 to 1004)
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247 c 232 g 265 t 6 others
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/db_xref-"taxon:9606"
/clone="IMAGE:5553194"
/clone="ib-"NIH_MGC_85"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cogburn, L.A. and Monsonego-Ornan, E.
ESTs from Normalized Chicken Breast Muscle, Leg Muscle,
Epiphyseal Growth Plate cDNA library, USDA/IFAFS Animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            University of Delaware Townsend Hall, Newark,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Larry A. Cogburn
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302-831-2822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cogburn@udel.edu, www.chickest.udel
               /note="Vector: pcMvSPORT6; Library made from equivalent pools of total RNA isolated from each tissue (embryonic muscle 33.3%; juvenile muscle 33.3%; and epiphyseal growth plate 33.3% of the final RNA pool). Single pass sequencing from 5'-end"

199 c 137 g 133 t
                                                                                                                                                                                                                                                        /clone-"pgm2n.pk005.j24"
/clone_lib-"Normalized Chicken Breast Muscle, Le
and Epiphyseal Growth Plate cDNA library (pgm2n)
/sex-"Male and Female"
                                                                                                                                                                                                               growth plate"
                                                                                                                                                                                                                                                                                                                                                                  /strain="Commercial broiler
Strains 90 & 21"
                                                                                                                                              /dev_stage="Breast,leg:Embryo(d19);post-hatch(1d,1,3,5,7,9
,11 weeks);growth plate(1d,7d,14d post-hatch)"
/lab_host="E. coli EMDH10B"
                                                                                                                                                                                                                                      /tissue_type="Breast muscle, leg muscle and epiphyseal
                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9031"
                                                                                                                                                                                                                                                                                                                                                                                                             ∕organism="Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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Query Match
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Matches 427; Conservative

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Score 329.2; DB 10; Pred. No. 4.4e-67; 0; Mismatches 163;

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                                                                                          CCCCGACTCGGGCAACACTCTCTACATCCTCACCACAAACGCATCCTCAAGTTCCTCAA 423
                                                                                                                       CAAAAAGCAGAGCTTTGTGGGCCATGCTGACCATCACTGACTTCATCAACATCCTGCACCG
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Search completed: October 3, 2002, 16:15:01 Job time: 16956 sec

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1: /cgn2_6/ptodata/2,

2: /cgn2_6/ptodata/2,

3: /cgn2_6/ptodata/2,

4: /cgn2_6/ptodata/2,

5: /cgn2_6/ptodata/2,

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length: 2000000000
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2000 Compugen
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
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Sequence 14, Application US/08878989
Patent No. 5885803
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl G.
APPLICANT: Guegler, Karl G.
APPLICANT: Lal, Preeti
APPLICANT: Goli, Surya K.
APPLICANT: Slah, purvi
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Query Match
Best Local Similarity
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SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                           567 tctacatgcgcttcatgcaggagcacacctgctacgatgccatggcaactagctccaagc
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NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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CLONE: 1452972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Incyte Pharmaceuticals, STREET: 3174 Porter Drive CITY: Palo Alto STATE: CA COUNTRY: USA
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REGISTRATION NUMBER: 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
                      accggatccatcgcctgctgttcttgacccggtgtcaggcaacgtactccacatcctca 986
ATAAAATCCACAGATTGCCCGTTATTGACCCTATCAGTGGGAATGCACTTTATATACTTA 602
                                                                                                                                                           agattgaacaacataagattgagacctggagggagatctacctgcaaggctgcttcaagc
                                                                  CTTTAGTGAATATCTCCAGATGCAAGCCTCTTCGATGCTGTATACTCCTTGATCAAAA
                                                                                       ctctggtctccatctctcctaatgatagcctgtttgaagctgtctacaccctcatcaaga
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Pred. No. 2.8e-87;
0; Mismatches 334;
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US-09-272-796-14
                                 STREET: 3174 POTTER DIVE

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARRE: FastSEO for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION: NUMBER: US/09/272,796
FILING DATE:
CLASSIFICATION: DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/878,989
                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 6207148
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 14,
                                                                                                                                                                                                                                                                                                        APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl G.
APPLICANT: Lal, Preeti
APPLICANT: Goli, Surya K.
APPLICANT: Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
     ATTORNEY/AGENT INFORMATION: NAME: Billings, Lucy J J
                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: DISEASE ASSOCIATED TITLE OF INVENTION: KINASES
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                              FILING DATE:
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3174 Porter Drive
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US-09-272-796-14
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Best Local Similarity 62.9%;
Matches 567; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PENITUTO1
CLONE: 1452972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                  agaggacactatgtctggagggagtcctttcctgccagccccacgagagcttgggggaag 1346
                                                                                                  acctggctgcccagcaaacctacaacctggacatgagtgtgggagaagccctgaggc 1286
                                                                                                                                                      ACCGTTCACAGTATTTTGAAGGTGTTGTGAAGTGCAATAAGCTGGAAATACTGGAGACCA
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Pred. No. 2.8e-87;
0; Mismatches 334;
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Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
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                                                                                                                                  Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMPLECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                      TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                             1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                          IMMEDIATE SOURCE:
924 agaaccggatccatcgcctgcttcttgacccggtgtcaggcaacgtactccacatcc 983
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                                                                                                             y Match 3.0%; So Local Similarity 2.6%; Prohes 10; Conservative 220;
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CITY: Alexandria
STATE: VA
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                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE:
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                                   agcctctggtctccatctccctaatgatagcctgtttgaagctgtctacaccctcatca 923
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1800 Diagonal Road, Suite 500
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                                                                                                                            Score 49; DB 1; Length 7218; Pred. No. 0.0021;
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                                                                                                           Mismatches 155; Indels
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CURRENT APPLICATION NUMBER: US/09/056,105
CURRENT APPLICATION NUMBER: 60/043,467
EARLIER APPLICATION NUMBER: 60/043,467
EARLIER FILING DATE: 1997-04-10
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 8
LENGTH: 1022
TYPE: DNA
ORGANISM: Homo Sapiens
US-09-056-105-8
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; Sequence 8, Application US/09056105

; Patent No. 6287569
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Best Local Similarity
Matches 160; Conserv
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APPLICANT: KIPPS, TH
APPLICANT: WU, YUNQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR TITLE OF INVENTION: PROCESSING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 233/221
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                                                                         aactagctccaagctagtcatcttcgacaccatgctggagatcaagaaggccttctttgc
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Pred. No. 0.12;
0; Mismatches 198; Indels 0
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Best Local Similarity 4.5%
Matches 12; Conservative
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TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                   1187
                     1307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                             1247
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APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: sing
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TELEFAX: (703)683-4109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Foley & Lardner STREET: 1800 Diagonal Road, Suite 500
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                                                     gccttgagatggacaaggcagaagtcggtggaggaaggggagccaccaggtcaggggaa 247
                                                                                           tggccatcaccagctgtgaccagcagctcagaaagaatccgtgggaaacggagggccaaa 187
                                                                                                                                                                       agccttgggggttctgagcatcaagagatgagcttcctagagcaagaaaacagcagctca 127
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                       2.4%; Score 40.2; DB 1;
4.5%; Pred. No. 0.44;
ative 150; Mismatches 103;
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Patent No. 5612201
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LENGTH: 1022
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Best Local Similarity
Matches 159; Conserv
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APPLICANT: WU, YUNQI
TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR
TITLE OF INVENTION: PROCESSING
TILE OF INVENTION: PROCESSING
TILE OF INVENTION: PROCESSING
CURRENT APPLICATION NUMBER: US/09/056,105
CURRENT FILING DATE: 1998-04-06
EARLIER APPLICATION NUMBER: 60/043,467
EARLIER APPLICATION NUMBER: 60/043,467
                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                       APPLICANT: De Plaen, Etienne; Boon-Falleur, Thierry; APPLICANT: Leth, Bernard; Szikora, Jean-Pierre; De APPLICANT: Chomez, Patrick
TITLE OF INVENTION: Isolated Nucleic Acid Molecules
                                                                   NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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STREET:
CITY: N
STATE:
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                                                     ADDRESSEE:
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             SEE: Felfe & Lynch
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New York City
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                                                                                                       Isolated Nucleic Acid Molecules Useful In Determining Expression Of A Tumor Antigen Precursor
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Pred. No. 0.31;
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Best Local Similarity 44.4%;
Matches 159; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                    1098 CCTGAAGATGATCTTTGGCATTGACGTGAAGGAAGTGGACCCCACCAGCAACACCTACAC 1157
                                                                                                                          1038 GAGAGTCATCAAAAATTACAAGCGCTGCTTTCCTGTGATCTTCGGCAAAGCCTCCGAGTC 1097
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613 aactagetecaagetagteatettegaeaceatgetggagateaagaaggeettettege 672
                                                                                                                                                                                                           978
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FILING DATE: 23-May-1991
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
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APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991
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APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
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                                                                                                                                                553 acceggegeceagatetaecatgegetteatgeaggageacacetgetaegatgecatgge 612
                                                                                                                                                                                                                                                                       918 CTCGCCTGACGCAGAGTCCTTGTTCCGAGAAGCACTCAGTAACAAGGTGGATGAGTTGGC
                                                                                                                                                                                                                                                                                             433 gttcccagccacagaggcctgggagtgtgagctagaaggcctgctggaagagaggcctgc 492
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APPLICATION NUMBER: 08/037,230
FILING DATE: 26-MARCH-1993
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REFERENCE/DOCKET NUMBER: LUD 53
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FILING DATE: 1-SEPTEMBER-1994
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9-JULY-1991
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Pred. No. 0.43;
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US-08-142-368A-14
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Best Local Similarity 44.4%;
Matches 159; Conservative
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                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 23-May-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5925729man D.
REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 07/728,838 APPLICATION NUMBER: 9-JULY-1991 PRIOR APPLICATION DATA:
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CURRENT APPLICATION NUMBER: US/08/142,368A
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LENGTH: 2531 base pairs
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PRIOR APPLICATION NIMBER: 07/764,364
433 gttcccagccacagaggcctgggagtgtgagctagaaggcctgctggaagagaggcctgc 492
                                                            858 CACTTGCTGGAGGCAACCCAATGAGGGTTCCAGCAGCCAAGAAGAAGAGGAGGGGCCAAGCAC 917
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APPLICATION NUMBER:
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APPLICATION NUMBER:
FILING DATE: 22-MAY-
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Boon-Falleur, Thierry; Van der Bruggen, Thierry; AppLICANT: Van den Eynde, Beno t; Van Pel, Aline; De Plaen, El APPLICANT: Lurquin, Christophe; Chomez, Patrick; Traversari, CTITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor TITLE OF INVENTION: Rejection Antigens and Uses Thereof
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12-DECEMBER-1991
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22-MAY-1992
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                                                                                                                                            Score 39.6; DB 2;
Pred. No. 0.43;
0; Mismatches 199,
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US-08-967-727-14
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                                                                                                        APPLICATION NUMBER: 07/705,702
FILING DATE: 23-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: HANSON, NO. 6025474man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5353
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
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                                                                       TELEFAX: (212) 838-3884 INFORMATION FOR SEQ ID NO:
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CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: 08/037,230
APPLICATION 26-MARCH-1993
FTIING DATE: 26-MARCH-1993
FTIING DATE: 26-MARCH-1993
                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                               APPLICATION NUMBER: 07/7:
FILING DATE: 9-JULY-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,365
FILING DATE: 23-SEPTEMBER-1991
                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US92/04
FILING DATE: 22-MAY 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991
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APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
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ADDRESSEE: Felfe & Lynch
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STRANDEDNESS:
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                                  LENGTH:
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                                2531 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14,
Patent No. 6
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991
                                                                                                                                                                                                                                                                     COMPUTER: IBM
OPERATING SYSTEM: PC-DC
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1158 CCTTGTCACCTGCCTGGGCCTTTCCTATGATGGCCTGCTGGGTAATAATCAGATCTTT 1215
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                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 26-MAF CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 805 Third Avenue CITY: New York City
                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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nes 159; Conserv
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6235525
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                                                                                                                                                                                                                                                                                                               PC-DOS
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FILING DATE: 23-MAY-1991 ATTORNEY/AGENT INFORMATION:

Hanson, No. 6235525man D.

PRIOR APPLICATION DATA:
APPLICATION NUMBER:

07/705,702

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APPLICANT: KIPPS, THOMAS J.

APPLICANT: WU, YUNQI
TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR
TITLE OF INVENTION: PROCESSING
FILE REFERENCE: 233/221
CURRENT APPLICATION NUMBER: US/09/056,105
CURRENT FILING DATE: 1998-04-06
EARLIER APPLICATION NUMBER: 60/043,467
EARLIER APPLICATION NUMBER: 60/043,467
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FASISEQ for Windows Version 3.0
SEQ ID NO 10
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                                                                                                                                                                                                                                                                                                                       Sequence 10, Applica Patent No. 6287569 GENERAL INFORMATION:
LENGTH: 4895
TYPE: DNA
ORGANISM: Homo sapiens
-09-056-105-10
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INFORMATION FOR SEQ ID NO: 14
SEQUENCE CHARACTERISTICS:
LENGTH: 2531 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local
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REFERENCE/DOCKET NUMBER: LU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEPAX: (212) 638-3884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1038 GAGAGTCATCAAAAATTACAAGCGCTGCTTTCCTGTGATCTTCGGCAAAGCCTCCGAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: genomic DNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        673 tctggtggccaacggtgtgcgggcagcccctctatgggacagcaagaagcagaagcttt 730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          858 CACTTGCTGGAGGCAACCCAATGAGGGTTCCAGCAGCAGAAGAAGAGGGGGGGCCAAGCAC 917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  373 ctctgactgtacagcctcagctgcaggctccagcacagatgatgtggagctggcacgga 432
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Local Similarity 44.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCTGAAGATGATCTTTGGCATTGACGTGAAGGAAGTGGACCCCACCAGCAACACCTACAC 1157
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                                                                                                                                                                                                                                                                                                                                                                  Application US/09056105
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NAME/KEY: misc_feature
LOCATION: (1)...(289)
OTHER INFORMATION: n -
US-09-007-005-17
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Best Local
                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 17, Application Patent No. 6258558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN TITLE OF INVENTION: FUSIONS FILE REFERENCE: 00786/350003 CURRENT APPLICATION NUMBER: US/09/007,005B CURRENT FILING DATE: 1998-01-14 EARLIER APPLICATION NUMBER: 60/035,963 EARLIER FILING DATE: 1997-01-27 EARLIER APPLICATION NUMBER: 60/064,491 EARLIER FILING DATE: 1997-11-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 159; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 28
TYPE: RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Szostak, Jack W.
                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Translation template
                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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186 NYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSY 127
                               954 acccggtgtcaggcaacgtactccacatcctcacacacaaacgcctgctcaagttcctgc 101:
                                                                                                3522 ccttgtcacctgcctgggcctttcctatgatggcctgctgggtaataatcagatcttt 3579
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                                                                      GYAYGYTYTYAYCYGYCYAYGYCYTYGYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSY 187
                                                                                                                                                         al Similarity
10; Conserv
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                                                                                                                                                       Conservative
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; Pred. No. 0.31;
87; Mismatches
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                                                                                                                                                     93;
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APPLICANT: SOSTER, Jack W.
APPLICANT: Roberts, Richard W.
APPLICANT: Liu, Rihe
TITLE OF INVENTION: EUSION OF PROTEINS USING RNA
TITLE OF INVENTION: FUSIONS
FILE REFERENCE: 00786/350007
CURRENT APPLICATION NUMBER: US/09/244,796
CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
EARLIER FILING DATE: 1997-11-06
EARLIER FILING DATE: 1997-11-06
EARLIER FILING DATE: 1998-01-14
SERILIER APPLICATION NUMBER: 09/007,005
EARLIER APPLICATION NUMBER: 05/077,005
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EARLIER FILING DATE: 1998-01-14
NUMBER OF SEO ID NOS: 33
SOSTWARE: FRASTSEQ for Windows Version 4.0
LENGTH: 289
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US-09-404-650-1
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: LOCATION: (1)...(289)
: OTHER INFORMATION: n = A,T,C
US-09-244-796-17
Sequence 1, Application US/09404650
Patent NO. 6309858
GENERAL INFORMATION:
APPLICANT: Dietrich, Paul S.
APPLICANT: MCGivern, Joseph G.
TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
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Best Local Similarity 5.3%; Pred. No. 0.31;
Matches 10; Conservative 87; Mismatches
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Patent No. 6281344
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US-09-404-650-1
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Best Local Similarity 47.5%;
Matches 115; Conservative
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FILE REFERENCE: RO0438-REG sequence listing
CURRENT APPLICATION NUMBER: US/09/404,650
CURRENT FILING DATE: 1999-09-23
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN VEY: 2.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens FEATURE:
                                                  4349 tgtgctcaacatgtttgtgggtgtcgtggtggagaacttccacaagtgccggcagcacca 4408
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Pred. No. 1;
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Search completed: October 3, 2002, 16:22:08 Job time: 16968 sec

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Minimum DB seq
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Perfect score:
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(c) 1993 - 2000 Compugen Ltd
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                          Description
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SOURCE
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Sequence 5 from Patent WO0177305.
AX281502
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                                                                                                                                                        Andersson, L., Luthman, H. and Marklund, S. Variants of the human amp-activated protein kinase gamma 3 subunit Patent: WO 0177305-A 5 18-OCT-2001;
                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Result No.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Characterization of AMP-activated protein kinase gamma-subunit isoforms and their role in AMP binding Blochem. J. 346 Pt 3, 659-669 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (12-OCT-1999) Carling D., Co
Clinical Sciences Centre, Hammersmith
London, W12 ONN, UNITED KINGDOM
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//db_xrefe"GI:16608834"
//db_xrefe"GI:16608834"
//tanslation-"medcleihalrrtpswsslaggsehoemsplegengsswpspavts
SSERIRGKRRAKALRWTROKSVEEGEPPGOGEGPRSRPAAESTGLEATFPKTTPLAQA
DPAGVGTPPTGWOCLPSUCTASAAGSSTODVELATEFPATEARECELEGLLEERPALC
LSPOAPPFKLGWDDELIKREGADIYMRFMQEHTCYDAMATSSKLVIFOTMLEIKKAFFAC
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GSLLPRSEFLYRTIOLALGIGTFROLAVULETAFLITALDIFVDRRVSALVENG
GSLLPRSEFLYRTOLGLIGTFROLAVULETAFLITALDIFVDRRVSALVENG
GSLLPRSEFLYRTOLGLIGTFROLAVULETAGLIFVDRECQV
VGLYSRFDVIHLAQQTYNHLDMSVGEALRQRTLCLEGVLSCQPHESLGEVIDRIARE
QVNRLVLVDETGHLGVVSLSULGALRQRTLCLEGVLSCQPHESLGEVIDRIARE
QVNRLVLVDETGHLGVVSLSULGALRQRTLCLEGVLSCQPHESLGEVIDRIARE
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LSPQAPFPKLGWDDLEKFGAQIYMRF1EEHTCYDAMATSSKLVIFDTMLEIKKAFFA
LVANGYRAAPIWDSKKQSFVGMLTTDFILVLHRYYRSPLVQIYEIRGHKIETWREIY
LVANGYRAAPIWDSKKQSFVGMLTTDFILVLHRYYRSPLVQIYEIRGHKIETWREIY
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/db_xref="taxon:9606"
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                                                                                                                                gggccaaagccttgagatggacaaggcagaagtcggtggaggaaggggagccaccaggtc
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Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE)
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VGLYSRFDVIHLAAQQTYNHLDMSVGEALRKRTLCLEGVLSCOPHESLGEVIDRIARE
QVHRLVLVDETOHLLGVVSLSDILQALVLSPAGIDPSGPEKI"
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ISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHKRLLKFLHIFGSLLPRPSFL
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     Mummalla: Eutheria: Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 2115)

Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M.,

Rogel-Gaillard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H.,

Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.

and Andersson,L.

A mutation in PRKAG3 associated with excess glycogen content in pic
                                                                                                                                                                                                         mRNA, con
AF214519
skeletal muscle
                                                                                                                                           Homo sapiens
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Homo sapiens AMP-activated pu
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Patent: WO 0120003-A 29 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA)
Andersson, Leif (SE); Looft, Christian (DE); Kalm,
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AX099802
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Rogel-Gaillard,C., Tannuccelli,N., Gellin,J.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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/db_xref="GI:13538837"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                     Andersson, L., Looft, C., Kalm, E., Milan, D., Rogel-Gaillard, C., Iannuccelli, N., Gellin, C.,
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Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A.,
Rogel-Gaillard,C., Paul,S., Gellin,J., Lundstrom,K.,
Kalm,E., Le Roy,P., Chardon,P. and Andersson,L.
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immalia; Eutheria; Cetartiodactyla; Suina; Suidae;
(bases 1 to 1867)
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/Product="AMP-activated protein kinase gamma subunit"
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/protein_id="AMP-activated protein kinase gamma subunit"
/db_xref="G1:8215682"
/translation="MSFLEQENSSWPSPAVTSSSERIRGKRRAKALRWTROKSPAGOTYM
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Pred. No. 4.1e-16;
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J., le
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Sus.
                                 (FR) ;
Ernst (DE)
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                                                                                                                                                                                            Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedis University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
                                                                                                                                                                                                                                    2 (bases 1 to 1873)
Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Rogel-Gaillard,C., Paul,S., Gellin,J., Lundstrom,K., Kalm,E., Le Roy,P., Chardon,P. and Andersson,L. Direct Submission
                                                                                                                                                                                                                                                                                                                                        skeletal muscle
Science 288 (5469), 1248-1251 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 1873)
Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M.,
Rogel-Gaillard,C., Paul,S., Tannuccelli,N., Rask,L., Ronne,H.,
Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pig.
Sus scrofa
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AF214520.1
                                                                                                                                                                                                                                                                                                                                                                                     A mutation in PRKAG3 associated with excess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF214520 1873 bp mRNA linear MAM 03-JUN Sus scrofa AMP-activated protein kinase gamma subunit (PRKAG3) mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota;
Mammalia;
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                                                                                                                 /organism="Sus scrofa"
/db_xref="taxon:9823"
/gene="PRKAG3"
                                                                                                                                                                   Location/Qualifiers
                              /gene="PRKAG3"
                                                  /tissue_type="skeletal muscle"
1. .1873
                                                                                    /map="15q"
                                                                                                    /chromosome="15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Cetartiodactyla; Suina; Suidae;
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TQHLLGVVSLSD1LQALVLSPAGIDALGA"
583 c 529 g 375 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="mhfmQeHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLTITDFILVLHRYYRSPLVQIYEIEEHKIETWREIYLQGCFKVLVS
ISPNDSLFEAVYALIKNRIHRLPVLDPVSGAVLHILTHKRLLKFLHIFGTLLPRPSFLYRTIQDLGITFRDLAVVLETAPILTALDIFVDRRVSALPVVNETGQVVGLYSRFDVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Sus scrofa"
/db_xref="taxon:9823"
472. .1389
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/db_xref="GI:13538809"
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Pred. No. 4.6e-09;
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Sus.
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Best Local 9
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61 agggggaaggtccccggtccaggccagctgctgagtccacc 101
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Sus scrofa
Eukaryota;
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Sequence 27
AX099800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      same, and uses thereof
Patent: WO 0120003-A 27 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR)
Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Variants of the gamma chain of ampk, dna sequences encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chardon, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rogel-Gaillard, C., Tannuccelli, N., Gellin, J., le Roy, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia;
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Similarity 82.2%;
83; Conservative
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dersson,L., Looft,C., Kalm,E., Milan,D., Robic,A.,
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HPWOEHTCVDAWATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKKOSFVGMLTI
TDFILVLHRYYRSPLVQIYEIEEHKIETWREIYLQGCFKPLVSISPNDSLFEAVYALI
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AVVLETAPLITADLIFFORDREWSALPVWNETGGVVGLYSRFDVIHLAAQGTVHLDMNV
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AVVLETAPLITADLIFFORDREWSALPVWNETGGVVGLYSRFDVIHLAAQGTVSHLDMNV
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ALVLSPAGIDALGA"
580 c 535 g
                                                     GEALRORTLCLEGVLSCOPHETLGEVIDRIVREQVHRLVLVDETQHLLGVVSLSDILQ
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/db_xref="taxon:9823"
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3 580 c 535 g
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HEMQETTCYDAMATSSKLVIFDTMLEIKAFFALVANGVRAAPLADSKKOSFYGMLTI
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AVVLETAPILTALDIFVDRRVSALPVVNETGQVVGLYSRFDVIHLAAQQTYNHLDMNV
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Pred. No. 4.6e-09;
0; Mismatches 18
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AX099804
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                                                                                                                                                                                                                                                                                                                                                                    236
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                                                                                                                                                                                                                                                                                                                    agggggaaggtccccggtccaggccagctgctgagtccacc 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.5%;
al Similarity 82.2%;
83; Conservation
                                                  Andersson, L., Luthman, H. and Marklund, S. Variants of the human amp-activated protein kinase gamma Patent: wo 0177305-A 2 18-OCT-2001;
                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae,
                                                                                                                                                                                                      Sequence 2 from Patent WO0177305
AX281579
                                                                                                                                                                                                                                                                                                                                                                                                                            83;
                                                                                                                                           Homo sapiens
                                            Arexis AB (SE)
                                                                                                                                                                                         AX281579.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Same, and uses thereof
Patent: wo 012003-A 31 22-MAR-2001;
INSTITUT MATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR);
Andersson, Leif (SE); Looft, Christian (DE); Kalm, Ernst (DE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chardon, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 31 from Patent Ax099804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A., Rogel-Gaillard,C., Tannuccelli,N., Gellin,J., le Roy,P. and
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∕organism≔"Homo sapiens"
                           Location/Qualifiers
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/db_xref="taxon:9823"
623 c 593 g
                                                                                                                                                                                      GI:16608830
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Pred. No. 4.5e-09;
0; Mismatches 18;
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Pred. No. 4.6e-09;
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                                                                                                             Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Karatas, A., Graham, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Karatas, A., Howland, J.C., Iliev, L., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Larocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McDwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McDwan, P., McGurk, A., McKernan, K., McPheeters, R., McHaldim, J., Maneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Morphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T. M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Starge-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Subraitssion
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                                                                                                                                                                                                                                                                                               Submitted (30-MAR-2000) whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA ON Jun 7, 2000 this sequence version replaced gi:7342115. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                        http://ftp.genome.washington.edu/RM/RepeatMasker.html
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71; Conserv
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1 (bases 1 to 152129)
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                                                          Center clone name:
                                                                                 Center project name:
                                                                                                                    Contact: sequence_submissions@genome
                                                                                                                                                            Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                            Center: Whitehead Institute/ MIT Center Center code: WIBR
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306 c 286 g
                             ne name: 504_G_11
Summary Statistics
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                                                                                                              Project Information
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; Pred. No. 1.1e-08;
...amatches 0;
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NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as soon as it
be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        insert size: 161000; agarose-fp
Insert size: 149029; sum-of-contigs
Quality coverage: 3.1 in Q20 bases; agarose-fp
Quality coverage: 3.3 in Q20 bases; sum-of-contigs
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Consensus quality: 135376 bases at least 040
Consensus quality: 143264 bases at least 030
Consensus quality: 146503 bases at least Q20
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3 85122: gap
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5 1285: contig of 4820 b
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38179: contig
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30170: contig of 3011 bp in
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33968: contig of 3698 bp in
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Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 6 On Nov 8, 2001 this sequence version replaced gi:13431203.
                                                                                                                                                                                                                        Waterston,R.H.
Direct Submission
Submitted (03-JAN-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
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Direct Submission
Submitted (08-NOV-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
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The sequence of Homo sapiens
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Sulston, J.E. and Waterston, R.
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Center project name: H_NH0459I19
                                Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                Center: Washington University Genome Sequencing Center Center code: WUGSC
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This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence restriction more than one subclone; and the assembly was confirmed by digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. MO. For additional information about the map position of this MO. For additional information about the map sequence, see http://genome.wustl.edu/gsc John L St. n D. et. Louis

SOURCE INFORMATION:

donor, as described by Osoegáwa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of becerial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute The RPCI-11 human BAC library was made from the blood of one male (http://bacpac.med.buffalo.edu)

pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-1077K22; the clone sequenced to the right is RP11-64705. Actual start of this sequences position 1 of RP11-459I19; actual end is at base position 206854 of RP11-459I19. clone

Data from AC079810 and AC073128 was used to finish this clone, AC009974. Polymorphisms have been identified between AC073128 AC009974. A single plasmid region exists between 38812-38903. unresolved tandem in the HERV SVA exists between 184390-185163. PCR suggests that approximately 1700 bps are missing. Location/Qualifiers ş

FEATURES source /organism="Homo sapiens" /db_xref="taxon:9606" 206854

misc_feature misc_feature misc_feature misc_feature misc_feature misc_feature misc_feature misc_feature misc_teature misc_feature misc_feature misc_feature misc_feature misc_feature /note="match to 281. .344 /note="match to 220. .221 /clone="RP11-459119" /clone_lib="RPCI-11" /note="match to /note="match to /note="similar to Homo sapiens
(NID:q14565249)" note="match to EST /note="match to /note="match to EST BG477625 (NID:g14565249) /note="match to EST BF304755 /note="match to EST AW880850 /note="match to EST AL567345 /note="match to /chromosome="2" note="match to EST BI059713 (NID:g14467240)" note="match to EST BE314060 (NID:g9134719)" /map=" EST EST EST BE047599 (NID:g8364652) tz39c01.y1" EST BF183086 BG470047 C05773 (NID:g1502549)* AI670836 (NID:g4850567) wa04g10.x1" BE908408 (NID: 913402322)* (NID:g10402954)" (NID: 98364652) tz39c01.y1* (NID:g13409904)" (NID:g11251653)* (NID: 98042860) * (NID: 912920610) (NID: g11061273)" EST BI114348

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap

between neighboring data submissions

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Query Match
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967. .1071
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684. .7
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                                                     /note="match to 967. .1091
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594...
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(NID:g14565249)"
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complement(557. .558)
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294. .3
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281. .3
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281. .3
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281. .344
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                                                                                                        .1084
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                                  AA043371 (NID:g1521226) zk53e10.rl*
                                                              BF304755
                                                                                     BE908408 (NID:g10402954)"
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Length 206854;
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Best Local Similarity 100.0%; Matches 71; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Assembly program: Phrap; version 0.990319
Consensus quality: 187795 bases at least 040
Consensus quality: 190513 bases at least 030
Consensus quality: 192099 bases at least Q20
Insert size: 200000; agarose-fp
Insert size: 200000; agarose-fp
Quality coverage: 5.8 in Q20 bases; agarose-fp
Quality coverage: 5.67 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing vector: plasmid; 0% chemistry: Dye-primer ET; 98% of reads chemistry: Dye-terminator Big Dye; 0% of the chemistry: Dye-terminator big Dye-terminator b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission

Direct Submission

Submitted (08-JUN-2000) Genome Sequencing Center, Washington

Iniversity School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: H_NH0647005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Washington University
Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    University School of Medicine, MO 63108, USA
On Feb 21, 2001 this sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      196554 bp DNA linear HTG 21-FEB-2001
Homo sapiens chromosome 2 clone RP11-64705, WORKING DRAFT SEQUENCE,
17 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequencing vector: M13; 98%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site:http://genome.wustl.edu/gsc/index.shtml
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Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
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HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                           arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Waterston, R.H
                                                                                                                                                                                                                                                                                                                                                       as soon as it is available and the accession number be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is
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1258
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1257: gap of
3600: contig
3700: gap of
5103: contig
5203: gap of
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contig of 2343 bp in length
gap of unknown length
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; Mismatches 0;
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of 1403
       unknown
of 3232
                                                                                   of 3321
                                                                                                                   unknown
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l bp in length
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Milan, D., Jeon, J.T., Looft, C., Amarger, V., Robic, A.,
Rogel-Gaillard, C., Paul, S., Gellin, J., Lundstrom, K.,
Kalm, E., Le Roy, P., Chardon, P. and Andersson, L.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish University of Agricultural Sciences, BMC Box 597, Uppsala 751 24,
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Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., The Rogel-Gaillard,C., Paul,S., Iannuccelli,N., Rask,L., Ron LundStrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L.,
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                                                                      /translation="MSFLEQGESRSWPSRAVITSSERSHGDQGNKASRWTRQEDVEEG
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HFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGHUTI
TDFILVLHRYYRSPLV0IYEIEBKKIEFWREIYLQGCKRPLVSISPNDSLFEAVYALI
KNRHIRLPVLDPVSGAVLHILTHKRLLKFLHTEGTLLPRSFLYRT10DLGIGTFFDL
KNRHIRLPVLDPVSGAVLHILTHKRLLKFHTEGTLLPRSFLYRT10DLGIGTFFDL
KNYLETAPLIFALDIFYDRRVSALPVVNETGQVVGLYSRFDVIHLAAQOTYNHLDMNV
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join(1. 154,515. 918,1809. 1890,2349. 2407,2509. 2554,2771. 2825,3027. 3153,3286. 3451,4578. 4615,4791. 4937,5294. 5410)
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2771. .2825,3027. .3153,3286. .3451,4578. .4615,4791. .4937,
5294. .>5410)
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                                                                                                                                                                                                                                                                                                                                                                                                         /product-"AMPK gamma
                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="PRKAG3"
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  (PRKAG3) gene, complete cds.
              3 others
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Sus.
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission

L Submitted (17-JAN-2001) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany

NOTE: This is a 'working draft' sequence. It currently

consists of 3 contigs. The true order of the pleces

is not known and their order in this sequence record is

rins of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence

as soon as it is available and the accession number will

be preserved.
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                                                     TGGGAGAAGGT 8780
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                                                                                                                         h 41.8%;
Similarity 74.6%;
53; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF336381 227724 bp DNA linear HTG 02-APR-2001 MUS musculus chromosome 1 clone PAC510; PAC457, *** SEQUENCING IN PROCRESS ***, 3 unordered pieces.
AF336381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 227724)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF336381.1 GI:13507298
HTG; HTGS_PHASE1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rump, A., Hayes, C., Brown, S.D.M. and Rosenthal, A. Mouse chromosome 1 genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
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17970
32747
32847
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/ 55423 c 56238 g 58199 t
                                                                                                                                                                                                                                                                                                                          1 17869: contig of 17869 bp in length 17969: gap of unknown length 0 32746: contig of 14777 bp in length 7 32846: gap of unknown length 7 227724: contig of 194878 bp in length Location/Qualifiers
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77.5%;
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Pred. No. 0.032;
0; Mismatches 16; Indels
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Search completed: October Job time: 12084 sec 3, 2002, 14:49:24

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1: /SIDS1/gcgdata/gcg.
2: /SIDS1/gcgdata/gcg.
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Comp
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240.868 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMAR	
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c 9	0 8	7	16	s	4	w	2	1	NO.	Result
31.8	31.8	71	72.2	72.2	72.2	99.4	99.4	101	Score	
31.5	31.5	70.3	71.5	71.5	71.5	98.4	98.4	100.0	Match	Ouerv
8670	8670	989	2022	1873	1867	2115	2109	1647	Match Length DB	
22	20	22	22	22	22	22	22	22	DB	
AAC90316	AAZ32059	AAH43682	AAD03321	AAD03319	AAD03295	AAD03320	AAD03296	AAH43685	ID	
X16619 cDNA clone.	Human METH2 relate	PRKAG3 intron 2 -	Sus scrofa PRKAG3	Pig AMPK gamma sub	Pig AMPK gamma sub	Human AMPK gamma s	Human AMPK gamma s	PRKAG3 cDNA. Homo	Description	

Nucleotide sequenc	AAH99921	24			7	5	c
Human mechanically	AAH78646	22			7.	44	C
Nucleotide sequenc	AAH99922	24			7.	43	a
Human h-TRAAK cDNA	AAA27106	21			27.8	42	c
Human mechanically	AAH78636	22			7.	41	c
	AAA27105	21			7	40	C
	AAL06997	22			28	39	O
Human ovarian and	ABA08137	22			28	38	O
Human polynucleoti	AA184199	22			28	37	o
DNA encoding novel	AAS43405	22	452		28	36	C
	AAS43330	22			28	35	
Human secreted pro	AAC58992	21				34	C
Human cDNA sequenc	AAH16987	22				ω W	c
	AAH68533	22	w		.80	32	
beta-globin	AAT48454	18			.00	31	
Human beta/gamma·g	AAA65169	21			.8	30	
Human secreted pro	AAC79994	21			.8	29	c
Corynebacterium gl	AAF72062	22			.80	28	c
C glutamicum codin	AAH67920	22			28.6	27	c
Portion of human b	AAQ83707	16			.8	26	
Human geta-globin	AAQ84934	16			.80	25	
Target sequence us	AAV41784	19			8	24	
5'-end of human be	AAT10719	17			8	23	
	AAX83492	20			8	22	C
	AAL02951	22			29	21	a
Human reproductive	AAL02949		_		29	20	a
Drosophila melanog	ABL12860		5981		29	19	
phila melano	286				N	18	o
polynucleot	AAK53283				9	17	a
polynucle	229				9	16	O
	AAV59752				29.4	15	C
	AAH14551				9	14	a
Human cDNA clone (AAH06841				9	13	ი
orter	0				29.8	12	
encoding	845	23	25	29.5	9.	11	
DNA encoding novel	AAS84420	23			30	10	

ALIGNMENTS

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RESULT
AAH43685
                                                                                                            CDS
                                                                                                                                              Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant; metabolic disease; diabetes; obesity; substitution; ss.
                                                                                                                                                                      PRKAG3 CDNA
                            variation
                                                          variation
                                                                                     variation
                                                                                                                                                                                    21-JAN-2002
                                                                                                                                                                                                   AAH43685;
                                                                                                                                                                                                                  AAH43685 standard; cDNA; 1647 BP.
                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                _
                                                                                                                                                                                   (first entry)
                                                         /note<del>-</del>
559
                            /note-
1037
            /*tag= d
/label= "C1037T"
                                                                                            /rtag= a
/product= "PRKAG3"
                                                                                                           Location/Qualifiers 20..1489
                                         /*tag= c
/label= "T559C"
                                                                       /label=
                                                                              /*tag= b
    "Causes R340W"
                                 "Silent variation"
                                                                "Causes P71A"
                                                                      "C230G"
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                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents the full length cDNA encoding the human AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution P71A; in exon 4 variation may be a substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution R71A of a three may also be variation in thron 6. The numbering of these variations is based on the full length cDNA as given, rather than on position 1 of the open reading frame.
                                                                       Homo sapiens
                                                                                                                                                                                                    13-JUN-2001 (first entry)
                                                                                                    cystathione beta
                                                                                                                                 PRKAG3;
                                                                                                                                                                        Human AMPK gamma
                                                                                                                                                                                                                                                               AAD03296 standard;
                                                                                                                  genetic testing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1647 BP; 346 A; 502 C; 462 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and refor determining a risk estimate of diseases in subject by detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-APR-2000; 2000US-195665P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-APR-2001; 2001WO-SE00765
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                                                                                                                                                                                                                                                                                                                                       240
                                                                                                                                                                                                                                                                                                                                              61 agggggaaggtccccggtccaggccagctqctgagtccacc 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                      1 999ccaaagccttgagatggacaaggcagaagtcggtggaggaaggggagccaccaggtc 60
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                                                                                                                                                                                                                                                                                                                                  agggggaaggtccccggtccaggccagctgctgagtccacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                         101;
                                                                                                                                       gamma subunit; adenosine monophosphate-activated kinase; AMPK;
                                                                                                           diabetes; obesity; myopathy; cardiovascular disease; anorec testing; carbohydrate metabolism disorder; skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Luthman
/*tag= a
472..1389
                            Location/Qualifiers
1..471
                                                                                                  synthase;
                                                                                                                                                                       subunit muscle-specific isoform,
                                                                                                                                                                                                                                                               DNA;
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                                                                                                                                                                                                                                                               2109
                                                                                                  CBS;
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Pred. No. 1.3e-20;
Pred. No. 1.3e-20;
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                                                                                               gene therapy;
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                                                                                                                                                                       PRKAG3 cDNA
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                      in a
of PF
                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is a cDNA encoding human adenosine monophosphate (AMP) activated kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle pRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are
AAD03320 standard; cDNA; 2115
                                                                                                                                                                                                                                                                                                                                                useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3. Transgenic animal and host cell transformed with PRKAG3 or a heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (INRG )
(ANDE/)
(LOOF/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of associated with energy metabolism such as diabetes, obesity,
                                                                                                                                                                                                                                                                                        Sequence
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Iannuccelli N,
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18-MAY-2000;
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                                                                          140 agggggaaggtccccggtccaggccaactgctgagtccacc 180
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                                                                                           61 agggggaaggtccccggtccaggccagctgctgagtccacc 101
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                                                                                                                                                        1 gggccaaagccttgagatggacaaggcagaagtcggtggaggaaggggagccaccaggtc 60
                                                                                                                                         gggccaaagccttgagatggacaaggcagaagtcggtggaggaaggggagccaccaggtc 139
                                                                                                                                                                                                                                                                                                                    sequence encoding the first cystathione beta synthase (CBS) RKAG3 and is useful in gene therapy.
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Gellin
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/product= "Human
1390..2109
                                                                                                                                                                                                                                                                                      458 A; 621 C; 560 G; 470 T; 0 other;
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99.08;
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J, Le Roy P, Chardon
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Pred. No. 4.1e-20;
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cc as diabetes, obesity, and disorders associated with muscle metabolism of control of the contr
    Query Match
Best Local Similarity
Matches 100; Conserv
                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                             useful as therapeutic for treating carbohydrate metabolism disorders such
                                                                                                                                                                                                                                                                                                                                                                                                                                               (AMP) activated kinase (AMPK) gamma subunit muscle-specific isoform, complete PRKAG3. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of associated with energy metabolism such as diabetes, obesity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 12; Page 65-68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ANDE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorec genetic testing; carbohydrate metabolism disorder; skeletal muscle;
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18-MAY-2000;
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PRKAG3 and
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2000EP-0401388
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4, Gellin
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1..1395
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Pred. No. 4.1e-20;
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Chardon P;
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     The present sequence is a cDNA encoding pig adenosine monophosphate (AMP) -activated kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3. Prkag3 gene is located in the RN locus of chromosome 15. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence activity, and for restoring a normal AMPK function. PRKAG3 sequence
                                                                                                                                                                       New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of associated with energy metabolism such as diabetes, obesity,
                                                                                                                                                                                                                                                               Claim 12;
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(ANDE/)
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18-MAY-2000;
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3; diabetes; obesity; myopathy; cardiovascular disease; (
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                                                                                                                                      Fig
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2000EP-0401388
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Gellin
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mutants are
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       scrofa
                                                                                                                                                                                                                                                                           Milan D,
                                                                                                                                                                                                                                                                ۵,
                                                                                                                                                                                                                                                               Chardon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRKAG3 protein"
useful for the
                                                                                                                                                                                                                                                               Robic A,
don P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101
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                                                                                                                                                                                                                                                                         Rogel-Gaillard C;
diagnostic
                                                                                                                                                                         disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anorectic;
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                            Pig: gamma subunit; adenosine monopnosphate accession disease; anorectic; PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; RN locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a genetic polymorphic marker linked to a sequence encoding PRRAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRRAG3. Transgenic animal and host cell transformed with PRRAG3 or a heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRRAG3 is useful for detecting mutations in a PrkaG3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.
New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment
                                              WPI; 2001-244810/25
P-PSDB; AAE00222.
                                                                                     Andersson L,
Iannuccelli N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD03319 standard;
                                                                                                                                            (ANDE/) ANDERSSON L. (LOOF/) LOOFT C.
                                                                                                                                                                                                     10-SEP-1999; 99EP-0402236
18-MAY-2000; 2000EP-0401388
                                                                                                                                                                                                                                               11-SEP-2000; 2000WO-EP09896
                                                                                                                                                                                                                                                                                                        WO200120003-A2
                                                                                                                                                                                                                                                                                                                                                                                                        Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pig AMPK gamma subunit muscle-specific isoform, complete PRKAG3 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    evaluation, genetic testing and prognosis of a metabolic dispreferably a carbohydrate metabolism disorder. Primers that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140 cgagggaaggtccccagtccaggccagttgctgagtccacc 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ggaacaaggcctctagatggacaaggcaggaggatgtagaggaagggggggcctccggggcc 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                     Looft C,
Gellin
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1..1395
                                                                                                                                                                                                                                                                                                                              /product= "Sus scrofa complete Prkag3
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82.2%;
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a
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Pred. No. 4.1e
0; Mismatches
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                                                                                   Roy
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by P, C
                                                                                   n D, Robic
Chardon P;
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4.1e-12;
hes 18;
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                                                                                                 Rogel-Gaillard
                                                                                                                                                                                                                                                                                                                              protein"
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of disorders
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PRKAG3, are
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뫄 Q Ъ QΥ

Query Match Best Local

Local Similarity

71.5%;

Score 72.2; DB Pred. No. 4.1e-1

DB 22;

Length 1873;

0

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complete PRKAG3. Prkag3 yene is located in the RN locus of chromosome

15. Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as cidabetes, obesity, and disorders associated with muscle metabolism contents such as suppathy and cardiovascular diseases, to modulate AMPK cardiovascular diseases, to modulate metabolism sequence and its functionally altered metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunctionally altered allele of PRKAG3, are useful for detecting and host cell transformed with PRKAG3 or a preferable candinal and host cell transformed with PRKAG3 or useful for screening compounds able to modulate AMPK activity. Nucleic actidence encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.
   Sequence 1873 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is a cDNA encoding pig adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                myopathy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 62-64; 71pp; English
382 A; 580 C; 535 G; 376 T; 0 other;
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RESULT
AAD03321
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                                                                                                                                                                                                                                                                                        Pig; gamma subunit; adenosine monophosphate-activated kinase; AMPK; PRKAG3; diabetes; obesity; myopathy; cardiovascular disease; anorec genetic testing; carbohydrate metabolism disorder; skeletal muscle;
 10-SEP-1999;
18-MAY-2000;
                                                                                                                                                                                                                                             Sus scrota
                                                    11-SEP-2000;
                                                                                        22-MAR-2001
                                                                                                                       WO200120003-A2
                                                                                                                                                                                                                                                                                                                                                               Sus scrofa PRKAG3 splice variant DNA.
                                                                                                                                                                                                                                                                                                                                                                                                   13-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ggaacaaggcctctagatggacaaggcaggaggatgtagaggaaggggggcctccggggcc 145
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99EP-0402236.
2000EP-0401388
                                                    2000WO-EP09896
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/product=
                                                                                                                                                                                        Location/Qualifiers
1..1545
                                                                                                                                                                                                                                                                           synthase;
                                                                                                                                                    "Sus scrofa Prkag3 splice
                                                                                                                                                                                                                                                                             CBS;
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                                                                                                                                                                                                                                                                         therapy;
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                                                                                                                                                                                                                                                                                                              anorectic;
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AAH43682
ID AAH4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CC diabetes, obesity, and disorders associated with muscle metabolism CC such as myopathy and cardiovascular diseases, to modulate AMPK CC activity, and for restoring a normal AMPK function. PRKAG3 sequence CC and its functionally altered mutants are useful for the diagnostic CC evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect CC a genetic polymorphic marker linked to a sequence encoding PRKAG3. are CC useful for detecting a dysfunction of carbohydrate metabolism resulting CC from the expression of a functionally altered allele of PRKAG3. are CC transgenic animal and host cell transformed with PRKAG3 or a CC neterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for CC screening compounds able to modulate AMPK activity. Nucleic acid CC encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or CC in a sequence encoding the first cystathione beta synthase (CBS) domain CC of PRKAG3 and is useful in gene therapy.
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Best L
                                                                                                                                                                                                                                                                                                                                                                           Matches
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(ANDE/)
(LOOF/)
 Key
                                                      Human; AMP-activated protein
metabolic disease; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is pig adenosine monophosphate (AMP)-activated kinase (AMPR) gamma subunit muscle-specific isoform, PRKAG3 splice variant DNA. Prkag3 gene is located in the RN locus of chromosome 15 Mutatlon in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as
                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of associated with energy metabolism such as diabetes, obesity,
                                                                                                PRKAG3 intron
                                                                                                                               21-JAN-2002
                                                                                                                                                                                     AAH43682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 12;
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Iannuccelli N,
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                                                                                                                                                                                                                                                                                                                               999ccaaagccttgagatggacaaggcagaagtcggtggaggaagggaggcaccaggtc
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ANDERSSON
LOOFT C.
KALM E.
                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                    standard;
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                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                            (first entry)
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Gellin
Location/Qualifiers
                                                                                                intron 4.
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                                                     kinase gamma 3 obesity; subst
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Pred. No. 4.1e-1
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                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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oy P, (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chardon
                                                      substitution;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  394
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don P;
                                                                    subunit;
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                                                                    PRKAG3; variant;
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RESULT 8
AAZ32059/c
ID AAZ32059

standard;

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AAZ32059

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Best Local S
Matches 71
                                                                                                                                                          is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution P71A; in exon 4 variation may be a substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution R340W. There may also be nucleotide variation in intron 6.
                                                                                                                                                                                                                                                          The sequences given in AAH43681-84 represents genomic encoding the human AMP-activated protein kinase gamma (PRKAG3). Detecting the presence of the PRKAG3 DNA, or
                                                                                                                                                                                                                                                                                                      Example 1;
                                                                                                                                                                                                                                                                                                                                 New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and me for determining a risk estimate of diseases in subject by detecting
                                                                                                                                                                                                                                                                                                                                                                              WPI;
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                                                                                                                                        Sequence 989
                                                                                                                                                                                                                                                                                                                          variant
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agggggaaggt
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                                      gggccaaagccttgagatggacaaggcagaagtcggtggaggaaggggagccaccaggtc
                                                 999ccaaagccttgagatggacaaggcagaagtcggtggaggaaggggagccaccaggtc
                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                     Fig
                                                                                   Conservative
                                                                                                                                        BP;
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178..541
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/*tag=
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                                                                                                                                        229
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                                                                                                                                                                                                                                   CC AAZ32000 and AAZ32001 encode, and AAY49501 and AAY49502 represent, human CC metalloprotease thrombospondin (MEPH) proteins METH1 and METH2 CC respectively. METH1 and METH2 have been found to be potent inhibitors of CC anglogenesis both in vitro and in vivo. They can be used for treating CC cancer and other disorders related to angiogenesis including abnormal CC wound healing, inflammation, rheumatoid arthritis, psoriasis, CC endometrial bleeding disorders, diabetic retinopathy, some forms of CC macula degeneration, haemangiomas, and arterial-venous malformations. CC They may be useful in treating deficiencies or disorders of the immune CC system, by activating or inhibiting the proliferation, differentiation, CC or mobilisation (Chemotaxis) of immune cells. The etiology of these CC immune deficiencies or disorders may be genetic, somatic, such as CC cancer or some autoimmune disorders, acquired (e.g. by chemotherapy or CC conditions, both chronic and acute conditions. The products can also be used to treat inflammatory CC used for detection and diagnosis. AAZ32002 to AAZ32080, and AAZ49501 to AAZ49501 to represent sequences given in the exemplification of the present CC invention.
                                                                                                                        Matches
                                                                                                                                      Query Match
Best Local :
 6522
                                                    6582 GAGGTGGAGGTGGCAGGAGGCGGTGGAGGTGGAGGCAGCGGTATCATGAAACAGCCC 6523
                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 431-437; 457pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated metalloprotease thrombospondin polypeptides, useful for treating hyperproliferative disorders, cancers or autoimmune disorde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (IRUE/) IRUELA-ARISPE L.
(HAST/) HASTINGS G A.
(RUBE/) RUBEN S M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-JAN-1998;
28-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rheumatoid arthritis; psoriasis; endometrial bleeding disorder; diabetic retinopathy; macula degeneration; haemangioma; detection; arterial-venous malformation; immune deficiency; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer; diagnosis; hyperproliferative disorder;
anglogenesis inhibitor; abnormal wound healing;
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                                                                      CCCGCCCAACCCCGC
                 ccggtccaggccagc
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                                                                                                                       Conservative
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98US-0098539
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                                                                                                                                                                                                1624 A;
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    anti-angiogenic; metalloprotease thrombospondin;
hyperproliferative disorder; autoimmune disease;

                                                                                                                                    31.5%;
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                                                                                                                                                                                                2421
                                                                                                                     0,:
                                                                                                                    Score 31.8; E
pred. No. 3.8;
0; Mismatches
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                                                                                                                    Indels
                                                                                                                                               Length 8670;
                                                                                                                                                                                               0
                                                                                                                                                                                           other;
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The present invention relates to human METH1 and METH2, (ME for metalloprotease and TH for thrombospondin; see AAB50002 and AAB50003). The present sequence is an expressed sequence tag (EST) for METH. METH can be used for inhibiting angiogenesis in an individual, and for treating cancer, benign tumours, an ocular angiogenic disease, rheumatoid arthritis, psoriasis, delayed wound healing, endometriosis, vasculogenesis, granulations, hypertrophic scars, nonunion fractures, scleroderma, trachoma, vascular adhesions, myocardial angiogenesis, coronary collaterals, cerebral collaterals, arteriovenous malformations, ischaemic limb angiogenesis, Osler-Webber syndrome, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, fibromuscular dysplasia, wound granulation, Crohn's disease or atherosclerosis. METH can also be used in birth control. METH can also be used in birth control. METH can also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-JUL-1999;
10-AUG-1999;
13-AUG-1999;
22-DEC-1999;
22-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              METH; metalloprotease; thrombospondin; angiogenesis inhibition; cancer therapy; benign tumour; ocular angiogenic disease; rheumatoid arthritis; psoriasis; wound healing; endometriosis; vasculogenesis; granulation; hypertrophic scar; nonunion fracture; scleroderma, trachoma; vascular adhesion; myocardial angiogenesis; coronary collateral; cerebral collateral; arteriovenous malformation; ischaemic limb angiogenesis; Osler Webber Syndrome; wound granulation; plaque neovascularisation; telangiectasia; haemophiliac joint; EST; angiofibroma; fibromuscular dysplasia; expressed sequence tag; crohn's disease; atherosclerosis; birth control; ss.
                                                                                                                                                                                                                                                                                    METH1 and METH2 polynucleotides and encoded polypeptides, used to inhibit angiogensis in the treatment of disorders such as cancer, rheumatoid arthritis and psoriasis -
                                                                                                                                                                                                                                                                                                                                                                                   Iruela-Arispe L,
Fornwald JA, Te
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IRUE/)
(HAST/)
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JONAK Z L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 TERRETT J A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BETH ISRAEL
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                                                                                                                                                                                                                                                             Pages
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99US-0144882.
99US-0147823.
99US-0373658.
99US-0171503.
                                                                                                                                                                                                                                                          731-737; 768pp; English.
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Sequence 8670 BP;

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1359 T; 0 other

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CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome complying and in recombinant production of (II). The convergence complying and in recombinant production of (II). The convergence complying and in recombinant production of (II). The convergence complying expressed genes. (I) is useful in gene therapy techniques convergence to restore mormal activity of (II) is useful in gene therapy techniques convergence to restore mormal activity of (II) or to treat disease states involving convergence to restore mormal activity of (II) or to treat disease states involving convergence conve
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AAS84420
ID AAS8
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Bost Local Similarity
Matches 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID No 20224; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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23-AUG-2000; 2000US-0649167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGGTGGAGGTGGCAGGAGGCGGTGGAGGTGGAGGCAGCGGTATCATGAAACAGCCC 6523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCCGCCCAACCCCGC 6508
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Pred. No. 3.
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CC quantitating a polypeptide in tissue, as molecular weight markers and as CC quantitating a polypeptide (II) sequences. (I) is useful as hybridisation probes, CC for identifying expressed genes. (I) is useful in gene therapy techniques (II). The polynucleotides are also used in diagnostics as expressed sequence tags (for identifying expressed genes. (I) is useful in gene therapy techniques (II). (II) is useful in gene therapy techniques (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as CC a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. (The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and CC amino acid sequences. AAS64197-AAS94564 represent novel human
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation of mutation of mathematics and to assess the second of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding novel
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upplement; medical imaging; diagnostic; genetic disorder; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20327; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human diagnostic protein #20327.
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Best Local S
Matches 46
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12-APR-2000; 2000US-196872P.
20-APR-2000; 2000US-199020P.
28-APR-2000; 2000US-205522P.
05-MAY-2000; 2000US-202348P.
11-MAY-2000; 2000US-203495P.
                                                                         Reddy R, Thornton M,
Gandhi AR, Yao MG, Sa
Policky JL, Yue H, Sa
Walsh RT, Lu DAM, Lu
Polypeptides of human transporters diagnosing, treating or preventing
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Note: The s
                                                                                                                                                                                                                                                                                                                                                                                                                                     Human: transporter and ion channel: TRICH: akinesia; cystic fibrosis; diabetes mellitus; Parkinson's disease; myasthenia gravis; dementia; cardiac disorder; angina; hypertension; myocarditis; hyperglycaemia; neurological disorder; Alzheimer's disease; cataract; infertility; wilson's disease; schizophrenia; Grave's disease; addison's disease; Huntington's disease; multiple sclerosis; meningitis; hypotensive; cardiant; nootropic; neuroprotective; neuroleptic; ophthalmological;
                                                                                                                                           (INCY-)
                                                                                                                                                                                                                                                                                                                                                                      CDS
                                                                                                                                                                                                                                                      06-APR-2001; 2001WO-US11206
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                                                                                                                                                                                                                                                                                                                                                                                                                                antithyroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human transporters and ion channels (TRICH)-12 cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12
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nes 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences.
                                          2002-017448/02
)B; AAE13285.
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                                                                                                                                          INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                              anticonvulsant;
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Hence data for this patent did not appear in the but was obtained in electronic format directly
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/product= "Human transporters
(TRICH)-12"
                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1..3933
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                                                                           M, Borowsky ML, T
Sanjanwala MS, E
Seilhamer JJ, Wa
Lu Y, Greene BD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA;
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Pred. No. 13;
0; Mismatches
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and ion channels, useful for disorders of transport,
                                                                     Tang YT, Khan FA, Tribou
Baughn MR, Nguyen DB;
Walia NK, Lal P, Kearney
WD, Raumann BE, Patterson C
                                                                                                                                                                                                                                                                                                                                                                                                                             antiinflammatory;
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                                                                                                                                                                                                                                                                                                                                         and ion channels
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RESULT 13
AAH06841/c
ID AAH068
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Best Local :
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                                                                                                      29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                  Ota T, I
Ishii S,
          WPI; 2001-318749/34
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                                                                             (HELI-) HELIX
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                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                   Human; primer;
                                                                                                                                                                                                                                                                                                                                                           26-JUN-2001
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                                  Isogai T,
, Sugiyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                       99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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                                                                                                                                                                                         2000EP-0116126
                                                                             RES
                                                                                                                                                                                                                                                                                               detection; diagnosis; antisense therapy; gene therapy;
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                                                                             INST
                                  Nishikawa
T, Wakama
                                                                                                                                                                                                                                                                                                                                                                                                               CDNA;
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                                    Wakamatsu
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                                 Hayashi K,
A, Nagai K,
                                                                                                                                                                                                                                                                                                                               IJ
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                                 Saito K,
Otsuki
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                                              Yamamoto
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AAH14551/c
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Best Local
                                                      29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                      07-FEB-2001
(HELI-) HELIX RES INST
                                                                                                                                                                                                                                                                                                                                                  EP1074617-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human cDNA sequence SEQ ID NO:12117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB92893 represent human amino acid sequences; and AAH13629 to AAH13632 represent invention.
                                                                                                                                                                                                                               28-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAH14551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3 'end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'end sequence/3'end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the complementary strand of a polynucleotide which comprises one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGAGAGAAGTCCCCGGGGCCAGCCTGC 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                            primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 58.(
51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
                                                   99JP-0248036.
99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                                                                                                                                                                                                               2000EP-0116126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      detection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           169 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA; 1457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 29.4;
Pred. No. 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                antisense therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36;
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CC The present invention describes primer sets for synthesising 5602 CC full-length cDNAs defined in the specification. Where a primer set CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary strand of a polynucleotide which comprises one of CC the 5602 nucleotide sequences defined in the specification, where the CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises at least 15 nucleotides; or (b) a combination of complementary strand of a polynucleotide which comprises a 5'-end cc complementary to an oligonucleotide comprising a sequence complementary to a complementary to an oligonucleotide comprises a 3'-end sequence complementary to a colynucleotide which comprises a 3'-end sequence, where the CC oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence's sequence, where the CC oligonucleotide comprises at least 15 nucleotides and the combination of the specification. The primer sets can be used in antisense therapy and CC in gene therapy. The primers are useful for synthesising polynucleotides, and perceivable of the comprises of the abnormality of the proteins encoded by the full-length cDNAs. The primers are also useful for the CC cDNAs easily without any specialised methods. AAH3166 to AAH3633 to AAH38742 represent human cDNA sequences; AAB92446 to CC AAB95893 represent human amino acid sequences; and AAH3629 to AAH3632 cof the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Primer sets for synthesizing full-length cDNAs defined in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ota T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ishii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001-318749/34.
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, Sugiyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID 12117; 2537pp + CD ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nishikawa
T, Wakam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polynucleotides, particularly the 5602 the specification, and for the detection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saito K,
Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yamamoto
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Sequence 1457 BP; 291 A; 442 C; 365 ç; 359 Η. 0 other;

present invention

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                                                                          Query Match
Best Local
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 40
                 62
                                             2 ggccaaagccttgagatggacaaggcagaagtcggtggaggaaggggagccaccaggtca 61
AGAGAGAAGTCCCCGGGGCCAGCCTGC
                gggggaaggtccccggtccaggccagc
                               Similarity
                                                                  Conservative
                                                                         29.1%;
                                                                 0
                                                                        Score 29.4;
Pred. No. 15;
                                                                 Mismatches
14
                88
                                                                                 DB
                                                                36;
                                                                                 22;
                                                                Indels
                                                                                Length
                                                                                1457;
                                                                0;
                                                                Gaps
                                                                0
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RESULT 15
AAV59752/c
ID AAV59752 standard; DNA; 1482
                                                       Human
                                                                  19-JAN-1999
                                                                           AAV59752;
                                                       secreted
                                                                (first entry)
                                                      protein gene 96 clone HAQBK61.
                                                                                   ВР
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Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclosteoporosis; arthritis; testis; lung; thyroiditis; thyroid; endocrine; metabolism; regulation; malabsorption; gastritis; osteoclast; thymus; neoplasm digestion;

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11 - APR 1997
23 - MAY 1997
24 - MAY 1997
25 - MAY 1997
27 - AUG 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-OCT-1997;
07-MAR-1997;
07-MAR-1997;
07-MAR-1997;
07-MAR-1997;
07-MAR-1997;
07-MAR-1997;
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07-MAR-1997;
11-APR-1997;
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11-APR-1997;
11-APR-1997;
11-APR-1997;
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11-APR-1997
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97US-0040162
97US-0040163
97US-0040334
97US-0040334
97US-0040336
97US-0043311
97US-0043313
97US-0043569
97US-0043569
97US-0043570
97US-0043571
97US-0043571
97US-0043572
97US-0047501
97US-0047583
97US-0047613
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-0040161
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This sequence represents a nucleic acid molecule designated Gene 96 from CD the human cDNA clone HADBK61 (deposited as clone ATCC 97897 and ATCC 209043) which encodes a secreted human protein. The gene can be used to CD generate fusion proteins by linking to the gene to a human CDMA clone proteins by linking to the gene to a human community of the fused protein as compared to the human protein only.

CC The invention relates to 186 novel genes and their fragments (nucleic acid sequences: AAV59511-V59812; amino acid sequences AAW74731-W75026) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological CC conditions can be diagnosed by determining the amount of the new CC polypeptides in a sample or by determining the amount of the 186 polynucleotides. Specific uses are described for each of the 186 polynucleotides, based on which tissues they are most highly expressed in (see AAV5951) for described uses).
                                                                                                                                                                                                                                                                                                                                                                                                                               Feng P, F
Kyaw H, L
Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-AUG-1997
                                                                                                                                                                                                                                                                                                               New isolated human genes and the secreted polypeptide(s) they encode - useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bednarik DP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN
                                                                                                                                                                                                                                                                                                                                                                                    1998-506364/43.
DB; AAW74967.
                                                                                                                                                                                                                                                                                      1; Page 478-479;
                                                                                                                                                                                                                                                                                                                                                                                                                          Ferrie AM, Fischer CL, Florenc
Lafleur DW, Li Y, Moore PA, 1
L, Shi Y, Soppet DR, Young PE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brewer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97US-0056909.
97US-0056910.
97US-00576591.
97US-0057650.
97US-0057669.
97US-0057761.
97US-0058785.
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97US-0056877
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97US-0056664
                                                                                                                                                                                                                                                                                   721pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                        Carter KC, Duan R, Ebner R, Endress GA her CL, Florence KA, Greene JM, Hu JS; Y, Moore PA, Ni J, Olsen HS, Rosen CA; DR, Young PE, Yu GL, Zeng Z;
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2 ggccaaagccttgagatggacaaggcagaagtcggtggaggaaggggagccaccaggtca 61

Query Match Best Local S Matches 51

l Similarity 51; Conserv

Conservative

0

36; 19;

Gaps

0

Score 29.4; D Pred. No. 15; 0; Mismatches

DB

Length Indels

1482; 0;

29.1%;

Sequence 1482

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ç; 368 <u>ن</u> 362

T:

other;

Search completed: October 3, 2002, 16:30:43 Job time: 14313 sec

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Title:
Perfect score:
Sequence:
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Maximum DB seq length: 2000000000
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Maximum Match 100%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OM nucleic - nucleic search, using sw model
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                            31
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Match
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ALIGNMENTS

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AUTHORS
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AW356079
LOCUS
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VERSION
                                                                       FEATURES
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                                                source
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Smith, T. P. L., Grosse, W. M., Freking, B. A., Roberts, A. J., Stone, R. T., Casas, E., Wray, J. E., White, J., Cho, J., Fahrenkrug, S. C., Bennett G. L., Heaton, M. P., Laegreid, W. W., Rohrer, G. A., Chitko-McKown, C. G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Reele, J. W.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                        BACKWARD: GTTTTCCCAGTCACGACG
Plate: 17 row: P column: 9
Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                 FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                       and -minmat
PCR PRimers
                                                                                                                                                                                                           Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -mins
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                          Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                              USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366
                                                                                                                                                                                                                                                                                                                                                                                                Contact: Smith TPL
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AW356079
AW356079.1 GI:6860085
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/organism="Bos taurus"
/db_xref="taxon:9913"
                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                            USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                         BACKWARD: GTTTTCCCAGTCACGACG Plate: 32 row: F column: 2
                                                                                                                                                                                                                                                                                                                                                                Single pass sequencing. Bases call v0.980904.e. Vector identified by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
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                                                                                                                                                                                                                                                                                                                                                                                                     Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Smith TPL
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63185 MARC 3BOV Bos taurus cDNA 5',
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                D
            /note="Vector: pCMV SPORT6; Site_1: xbaI; Site_2: xhoI; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and feti longissimus muscle."

136 c 125 g 59 t
                                                                                                                                              /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
                                                                                                             /tissue_type="pooled"
/lab_host="DH10B"
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a 126 c 117 g 56 t
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/tissue_type="pooled"
/lab_host="DH10B"
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79.2%;
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No. 1.8e-07;
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                                                                                                                                                     Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Yamanaka, I. Kiyosawa, H., Kondo, S., Saito, T., Shihagawa, A., Aizaw, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., Arakawa, T. Ishii, Y. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: genome-res@gsc.riken.go.jp,

ORL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi,K., Fujiwake,S., Inoue,K., Togawa,K., Taawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Sakoi,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
                                                                                                                Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct. Func. Genomics 2 pre, L72-L86 (2001
                                                                                                                                                                                                                                                                                                                                                         RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
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                                                                   further details
                                                                                                                                                                                                                                                                                                                                                                                                                                          Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fax: 81-45-503-9216
                                         e mouse tissues
                                                                                      Please visit our
                                                                                                                                                                                                                                                                                                                 Y. and Hayashizaki,Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T.,
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RIKEN full-length enriched, 16 days neor
cDNA clone 9630039L22 5', mRNA sequence
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79.28;
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Rodentia;
                                                                                        site
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Pred. No. 1.8e-07;
                                                                                                                                                                                                                                                                                                                            Shibata, K., Itoh, M., Carninci, P., Sugahara
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                                                                                 (http://genome.gsc.riken.go.jp) for
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                                                                                                                                                                                    Arakawa, T.,
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SOURCE
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ORIGIN
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Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda Okazaki, C., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, C., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, X., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, T., Olio, T., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, T., Olio, T., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, T., Paramit was a shanaka wangawa, A., Shiraki, T., Sogabe, Y., Suzuki, T., Paramit wangawa, A., Shiraki, T., Sogabe, Y., Suzuki, T., Paramit wangawa, A., Shiraki, T., Sogabe, Y., Suzuki, T., Paramit wangawa, A., Shiraki, T., Sogabe, Y., Suzuki, T., Paramit wangawa, A., Shiraki, T., Sogabe, Y., Suzuki, T., Paramit wangawa, A., Shiraki, T., Sogabe, Y., Suzuki, T., Paramit wangawa, A., Shiraki, T., Sogabe, Y., Suzuki, T., Paramit wangawa, A., Shiraki, T., Sogabe, Y., Suzuki, T., Paramit wangawa, A., Shiraki, T., Sogabe, Y., Suzuki, T., Paramit wangawa, A., Shiraki, T., Sogabe, Y., Saramit wangawa, A., Shiraki, T., Saramit wangawa, A., Shiraki, T.,
                                                                        Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-Tel: 81-45-503-9212
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                         Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BB629521 RIKEN full-length enriched, adult male bone cDNA clone 9830138C07 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone~"9630039L22"
/clone_lib~"RIKEN full-length enriched, 16 days neonate
cerebellum"
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/lab_host="DH10B"
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/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tagawa, A., Takahashi, F., Takeda, Y.,
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Pred. No. 2e-07;
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                                                                                              324 TGGGAGAAGGTGCCCAGTCCAGACCAGCTGCTGAGTCCACC
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e mouse tissues.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Site_1: Sall; Site_2: BamHI; cDNA library was
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/db_xref="taxon:10090"
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/dev_stage="adult"
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79.2%;
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Pred. No. 2e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001), Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizav, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
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Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0
Tel: 81-45-503-9222
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RIKEN Mouse ESTS (Arakawa, T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    further details
e mouse tissue
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                                                                                     prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-leng cap-trapper. cDNA went through one round of normalizations.
                                                                                                                                                                                                                                                                                                                                                /tissue_type="skin"
/dev_stage="6 days neonate"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="A030014A04"
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Rodentia;
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enriched for full-length b one round of normalization
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467815 MARC:
BI775360
BI775360.1 (
                                                                                                                                                                                                                                                                                                          Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscor
                                                                                                                                                                                                            BACKWARD: GTTTTCCCAGTCACGACG
Plate: 90 row: I column: 16
Seq primer: ATTTAGGTGACACTATAG
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PO Box 166, Clay Center, NE 68933-0166,
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                    and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
                                                                                                                                                                                                                                                                    FORWARD: AGGAAACAGCTATGACCAT
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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/note="Vector: pCMV SPORT6; Site_1: xba1; Site_2: xho1; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."

173 c 163 g 93 t
                                                                                      /tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                      /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
                                                                                                                                                                                             Location/Qualifiers
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IMAGE:1970001
A1664508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 484.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
Other_ESTs: uk25b05.x1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 516)
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: custom primer used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGI:986741
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314 286 1810
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                                                                                     insert. Size selection was performed to exclude fragments (41.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."
                                                                                                                                                                                   /note="Vector: PME18S-FL3; Site_1: DraIII (CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA
                                                                                                                                                                                                                                                                                                          /clone_11b="Sugano mouse embryo mewa"
/dev_stage="embryo, 14 dpc"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                 /strain="C57BL"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE: 1970001"
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Sugano mouse embryo mewa Mus
901 5', mRNA seguence
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            Score 53
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Pred. No. 0.00033;
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gctgctgagtccacc 101
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Best Local Similarity Matches 78; Conserv
                                                                                                                                 Local Similarity
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                             cagaagtcggtggaggaaggggagccaccaggtcagggggaaggtccccggtccaggcca 86
gggccaaagccttgagatggacaaggcagaagtcggtggaggaaggggagccaccaggtc
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Plate: 57 row: H column: 11
Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: smith@email.marc.usda.gov
Single pass sequencing. Hases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 444)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FORWARD: AGGAAACAGCTATGACCAT
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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                                                                                                                                                                                                                                                 /tissue_type="pooled"
/lab_host="DHIOB"
/lab_host="DHIOB"
/note="Vector: pcMv SPORT6; Site_1: XbaI; Site_2: XhoI;
/ibbrary made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendonosus muscle, and fetal
longissimus muscle."
a 147 c 139 g 67 t
                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
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81.3%;
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                                                                                                    Score 52.6; DB 10;
Pred. No. 0.00099;
0; Mismatches 14;
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BI754053/c
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                                                                                                                                                                                                                                                                                                        915 CGACAGGTTTGCCCCCGGATGGGTTCGAATTCCCAGGTGGGACTGGAGCCAACAGGGCCCT 856
                                                                                                                                                                                                                                                        64 gggaaggtccccggtccaggccagctgctg 93
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                                                                        406 bp mRNA linear
BB759831 RIKEN full-length enriched, melanocyte Mus
clone G270121L23 3', mRNA sequence.
BB759831
Mus musculus
                                                     BB759831.1 GI:16206159
                  house mouse
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Plate: LLAM11495 row: n column: 01
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Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
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/db_xrefe"taxon:9606"
/clone="IHAGE:5198016"
/clone_lib="NHH_MGC_114"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-*Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: EccRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dT primed and directionally cloned (EccRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                             Score 35.6;
Pred. No. 23;
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Best Local
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                                                                                                                                                                                                       197 CAGGGACCCCGAGCAGGTCTGCTATCAAGTTCAGC
                                                                                                                                                                                                                                    67 aaggtccccggtccaggccagctgctgagtccacc 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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                                                                                                                                                                                                                                                                                                         AAGCCCTGAGTTCCCCAAGCAGAAGGCAGGGGGGGGAGAAAGGCAGAGGCCAGAGTGGGAGG 198
                                                                                                                                                                                                                                                                                                                                            aagccttgagatggacaaggcagaagtcggtggaggaaggggagccaccaggtcaggggg 66
BB780864 ATKEN full-length enriched, colon RCB-09 musculus cDNA clone G430068010 3', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details. e mouse tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: genome res@gsc.riken.go.jp,

RI:http://genome.gsc.riken.go.jp,

Carninci.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,

Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura, S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T.,
Hayatsu, W., Hiramoto, K., Hiracka, T., Hirozane, T., Imotani, K., Ishii,
Y. Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T.,
Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T.,
Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K.,
Saito, R., Sakai, C., Sakai, T., Sogabe, Y., Suzuki, H., Tagawa
, A., Takahashi, F., Takaku-akahira, S., Tanaka, T., Tomaru, A., Toya, T.,
Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 58.9
56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
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Contact: Yoshihide Hayashizaki
Caboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
/clone="G270121L23"
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Pred. No. 1.1e+02;
0; Mismatches 39;
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                               mRNA linear
d, colon RCB-0549
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        253
                                                                                          313 AAGCCCTGAGTTCCCCAAGCAGAAGGCAGGAGGGAGAAAGGCAGAGGCCACAGTGGGAGG 254
                                                         67
                                                                                                                                                                                                                                      Local
                                                                                                                              AAGGGACCCCGAGCAGGTCTGCTATCAAGTTCAGC 219
                                aaggtccccggtccaggccagctgctgagtccacc 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Computer based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci.p., Shibata,Y. Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
N., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
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hayashizaki,Y.
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Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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/clone="G43068010"
/clone_lib="RIKEN full-length enriched, colon RCB-0549
Cle-H3 CDNA"
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                                                                                                                                                                                                                                                                                                                                                         /tissue_type="colon"
/cell_line="RCB-0549 Cle-H3"
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                                                                                                                                                                                                                                   32.3%;
58.9%;
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Pred. No. 1.1e+02;
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Best Local
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                                                                                                                                                                                                                                                          62 gggggaaggtccccggtccaggccagc 88
                                                                                                                                                                                                                                       53 AGAGAGAAGTCCCCGGGGCCAGCCTGC
                                                                                                                                                                                                                                                                                                                                    BG244994
BG244994.1 GI:12754809
                                                                                         mRNA sequence.
                                                                                                       BG244994 151 bp mRNA linear EST 13-FEB-: 602358260F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:4486719
                                                                                                                                                                                                                                                                                                                                                                                                l Similarity 60.9
53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11465 row: h column: 16
High quality sequence stop: 736.
Location/Qualifiers
                   house mouse
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Tissue Procurement: Life Technologies,
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 736)
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BI765906.1 GI:15757484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: pooled colon, kidney, stomach: Vector: pCMV-SPOR76; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="IMAGE:5186367"
/clone_lib="NIH_MGC_116"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                   32.3%;
                                                                                                                                                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                                                                                                                             Score 32.6; DB 10
Pred. No. 1.2e+02;
0; Mismatches 34
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#AGE:4486719 5',
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Mus musculus

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KEYWORDS
SOURCE
ORGANISM
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BB860266
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Best Local Similarity
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGGTGGACTCGGCAGACGCCGGTGGAGGGTGAGGATCACCCGGGAAGGGGGGGACGACG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gagatggacaaggcagaagtcggtggaggaaggggagccaccaggtcagggggaaggtcc 73
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                                                                         Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shinaski, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45;
                          Unpublished (2001)
                                                                  RIKEN Encyclopedia
                                                                                                                                                                                                                                                                          Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                  BB860266 RIKEN full-length enriched, pooled cDNA clone G430012004 5', mRNA sequence. BB860266
                                                                                                                                                                                                                                                                                                                                                                 house mouse.
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Location/Qualifiers
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10330 row: h column: 16
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Tissue Procurement: Gilbert Smith, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases i to 151)
NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian
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Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae;
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Yoshihide Hayashizaki
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3 8 c 70 g 22 t
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/clone="IMAGE:4486719"
/clone_lib="NCI_CGAP_Maml"
/tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="FVB/N"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32.1%;
68.2%;
                                                             of Mouse Full-length cDNAs (Akimura, T., et al.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           454 bp
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                                                                                                                                                                                                                                                                                                          66
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                                                                                                                                                                                                                                                                                                    gaaggtccccggtccaggccagctgctg 93
BF549656 479 bp mRNA linear UI-R-C2-ng-f-01-0-UI.rl UI-R-C2 Rattus norvegicus UI-R-C2-ng-f-01-0-UI 5′, mRNA sequence.
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wagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hayashizaki,Y.
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URL:http://genome.gsc.riken.go.jp/
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1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e mouse tissues.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="RIKEN full-length enriched, pooled cell lines"
/note="pooled cell lines; (cell_line=RCB-1754 WEHI 164),
(cell_line=RCB-01646 Weth-1764),
(cell_line=RCB-0464 Weth-A), (cell_line=RCB-035 WEHI-3),
(cell_line=RCB-0559 K-1 Fl), (cell_line=RCB-1283 B16

melanoma), (cell_type=B cells, cell_line=CRL-1702 WEHI 231
), (cell_type=Leydig cells, cell_line=CRL-2056 MLTC-1),
(cell_type=Mullipotent stem cell, cell_line=CRL-2070 NE),
(tissue_type=bladder, cell_line=RCB-0544 MBT-2),
(tissue_type=bladder, cell_line=RCB-0544 MBT-2),
(tissue_type=bladder, cell_line=RCB-0540 MCC-1),
cell_line=CRL-2028 SR-4987), (tissue_type=colon,
cell_line=CRL-9049 Cle-H3), (tissue_type=kidney,
cell_line=CRL-1734 SCA-9 clone 15), (strain=BALB/C,
cell_line=CRL-1734 SCA-9 clone 15), (strain=BALB/C,
cell_line=CRL-1734 SCA-9 clone 15), (strain=BALB/C,
cell_type=B cells, cell_line=CRL-1669 BCL1 Clone 13.20-3B3
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Pred. No.
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                                                   cDNA clone
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AUTHORS
TITLE
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Best Local Similarity 62.5%;
Matches 50; Conservative
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108 AGAGCCCTGGCCAAGGCAGC
                                                                69 ggtccccggtccaggccagc 88
                                                                                                                        48 GACTTGGGCTGCACAAGGCACCAGAGCGTGCAGACTGAGGATGGCCCAGGTGGGGTGGCC 107
                                                                                                                                                                  9 gccttgagatggacaaggcagaagtcggtggaggaaggggagccaccaggtcagggggaa 68
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Fax: 319 335 9265

Email: msoares@blue.weeg.utowa.edu

cDNA Library Preparation: M.B. Soares Lab Clone distribution:

clones will be available through Research Genetics (www.resgen.com)

This clone is also available through the I.M.A.G.E. Consortium at

LLNL (info@image.linl.gov). IMAGE ID= 1776352

Seq primer: M13 Forward.
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Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Res. 6 (9), 791-806 (1996) 97044477
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus
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//dev_
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/clone_lib="UI-R-C2"
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/db_xref="taxon:10116"
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/strain="Sprague-Dawley"
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127
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Pred. No. 1.6e+02;
0; Mismatches 30; Indels
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Search completed: October 3, 2002, 16:15:04 Job time: 16959 sec

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Minimum DB :
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Maximum Match 100%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Searched:
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                                seq length: 0 seq length: 2000000000
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*
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Gapop 10.0 , Gapext 1.0
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                   US-09-404-650-12
US-08-76-859-1
US-08-776-859-1
US-08-776-859-1
US-08-826-532-1
US-08-826-532-1
US-09-228-324A-1
US-09-138-922-3
US-08-105-989-3
US-08-105-989-53-2
US-08-164-2928-15
US-08-164-2928-17
US-08-164-2928-21
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US-08-815-623-17
US-08-845-623-17
US-08-845-623-21
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US-08-845-623-25
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; TYPE: DNA
; ORGANISM: Rattus s
US-09-404-650-12
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US-08-800-840-1
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PCT-US95-02689-51	US-08-207-481-44	US-US-343-443H-9/	115-09-343-4435-07	5449756-1	5198359-1	US-09-103-840A-1	US-09-103-840A-2	US-09-328-111-464	US-09-103-330-35	08-09-103-330-25	05-09-103-330-23	10 - 00 - 100 000 000 000 000 000 000 00	US-09-103-330-21	US-09-103-330-19	US-09-103-330-17	US-09-103-330-15	US-08-815-927-25	US-08-815-927-23	US-08-815-927-21	
Sequence 51, Appl		Sequence 97, Appl	-		Patent No. 5198359		2	464	35	Sequence 25, Appl	Sequence 23, Appl	seductice 51' Who	2 ;	9	17	15	Sequence 25, Appl	Sequence 23, Appl	Sequence 21, Appl	

ALIGNMENTS

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Sequence 12, Application US/09404650
Patent No. 630988
GENERAL INFORMATION:
APPLICANT: Dietrich, Paul S.
APPLICANT: MCGIVERN, JOSEPH G.
TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
TITLE OF INVENTION: AND USES
FILE REFERENCE: R0043B-REG sequence listing
CURRENT APPLICATION NUMBER: US/09/404,650
CURRENT APPLICATION NUMBER: US/09/404,650
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
                                                                                                                                                                                                                                        Sequence 1, Application US/08800840 Patent No. 6060288
                         GENERAL INFORMATION:

APPLICANT: Adams, Christopher P.

APPLICANT: Boles, Truett C.

APPLICANT: Muir, Andrew R.

APPLICANT: Kron, Stephen J.

TITLE OF INVENTION: Method and Apparatus for Performing
TITLE OF INVENTION: Amplification of Nucleic Acis on Supports
NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                              5474 CACAGGGGCAGGGGCAGGGGCAGGGCAGGGACCAGGGGCCAGGGGCCAGGGGCCGA 5415
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                    ADDRESSEE: Hamilton, Brook,
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Two Militia Drive
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Pred. No. 4.1;
                  Smith & Reynolds,
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COMPUTER READABLE FORM:

COUNTRY:

STATE: Massachusetts

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                                                                         SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08776859 Patent No. 6090592
LENGTH: 268
TYPE: DNA
ORGANISM: Homo sapiens
-08-776-859-1
                                                                                   FILE REFERENCE: MOSAIC
CURRENT APPLICATION NUMBER: US/08/776,859
CURRENT FILING DATE: 1997-05-29
EARLIER APPLICATION NUMBER: 08/285,385
EARLIER FILING DATE: 1994-03-08
NUMBER OF SEQ ID NOS: 4
SOFTMARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                             APPLICANT: Mosaic Technologies, Inc.
APPLICANT: Adams, Christopher P.
APPLICANT: Kron, Stephen J.
TITLE OF INVENTION: Method and Apparatus for Performing
TITLE OF INVENTION: Amplification of Nucleic Acids on Supports
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Best Local S
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REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: MST9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 617-861-9540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 268 base pairs
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FILING DATE: 03-AUG-1994
PRIOR APPLICATION NUMBER: PCT/US95/09905
FILING DATE: 03-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 03-FEB-1997
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                               110 TGGGCATAAAAGTCAGGGCAGAGCCATCTATTGCTTACA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 agggggaaggtcccccggtccaggccagctgctgagtcca 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/800,840 FILING DATE: 14-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Pred. No. 2.6;
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Best Local S
Matches 55
                                                                       Query Match
Best Local
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                        TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                             HYPOTHETICAL: NC
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homc
                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/285,385 FILING DATE: 03-AUGUST-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US95
FILING DATE: FILED HEREWITH
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/28
                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 29,809
REFERENCE/DOCKET NUMBER: BO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
             STRANDEDNESS:
                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                          NAME: JANIUK, ANTHONY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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                                                        l Similarity 55.6
55; Conservative
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55; Conservative
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                                                                                                                                           Homo sapiens
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                                                                       28.3%;
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                                                      Score 28.6; DE Pred. No. 2.6; 0; Mismatches
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                                                        Indels
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, TYPE: DNA
; ORGANISM: Homo sapions
US-08-826-532-1
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                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 428
                                                                                                                                       Matches
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Best Local Similarity
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Best Local Similarity
Matches 55; Conserv
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TITLE OF INVENTION: Linked Linear Amplification of Nucleic Acids
FILE REFERENCE: 3239-102P
CURRENT APPLICATION NUMBER: US/08/826,532B
CURRENT FILING DATE: 1997-04-02
EARLIER APPLICATION NUMBER: US 08/475,605
EARLIER FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 20
SOUTWARE: Patentin Ver. 2.0
SEQ 1D NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 08/826,532
PRIOR FILING DATE: 1997-04-02
NUMBER OF SEQ ID NOS: 64
                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/228,324A CURRENT FILING DATE: 1999-01-11
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Reyes, Antonio A
APPLICANT: Wallace, Robert B.
APPLICANT: Ugozzoli, Luis A.
TITLE OF INVENTION: Linked Linear Amplification of Nucleic Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 3239-103P
                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
     73
               61 agggggaaggtccccggtccaggccagctgctgagtcca 99
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                                                                           999ccaaagccttgagatggacaaggcagaagtcggtggaggaaggggagccaccaggtc 60
                                                          tgggcataaaagtcagggcagagccatctattgcttaca 111
                                                                                                                                  Conservative
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                                                                                                                                                28.3%;
55.6%;
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                                                                                                                               Score 28.6; DB 4; Length 428;
Pred. No. 2.8;
0; Mismatches 44; Indels
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Pred. No. 2.8;
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US-08-105-989-3
                                                                                                                                           Sequence 3, Application US/09138922 Patent No. 6147202
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                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                            APPLICANT: Kumar, Ramesh
APPLICANT: Sharma, Ajay
APPLICANT: Paulhiao, Cilara
APPLICANT: Khoury-Christianson, Anastasia P.
APPLICANT: Midha, Sunita
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 596 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/105,989
FILING DATE: 11-AUG-1993
CLASSIFICATION: 800
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kumar, Ramesh
APPLICANT: Sharma, Ajay
APPLICANT: Paulhiac, Clara
APPLICANT: Khoury-Christianson, Anastasia P.
APPLICANT: Midha, Sunita
TITLE OF INVENTION: Production of Human Hemoglobin in
TITLE OF INVENTION: Transgenic Pigs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: COPUZZÍ, LAURA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 679
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                  491 TGGGCATAAAAGTCAGGGCAGAGCCATCTATTGCTTACA 529
                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                61 agggggaaggtccccggtccaggccagctgctgagtcca 99
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STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : (212) 790-9090
(212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Production of Human Transgenic Pigs.
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Pred. No. 3;
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               Hemoglobin in
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NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS:

STATE: New York

New York

STREET: ADDRESSEE:

1155 Avenue of the Americas

PENNIE & EDMONDS

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US-08-550-715-10
: Sequence 10, A
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Best Local Similarity
Matches 55; Conserv
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FILING DATE: 11-AUG-193
ATTORNEY/AGENT INFORMATION:
NAME: COFUZZI, LAUFA A.
REGISTRATION NUMBER: 30,742
REFERENCE/JOCKET NUMBER: 6794-030
TELEPHONE: (212) 790-9990
TELEPHONE: (212) 790-9990
                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                  tent No.
                                                                                                                                                                                                                       TITLE OF INVENTION:
CURRENT APPLICATION DATA:
                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 596 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                      491 TGGGCATAAAAGTCAGGGCAGAGCCATCTATTGCTTACA 529
                                                                                                                                                                                                                                                                                                                                                                                                                                          431
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                                                                                                                            CITY: Chicago
STATE: Illino
                                                                                            ZIP: 60606-6402
                                                                                                           COUNTRY:
                                                                                                                                                        STREET:
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                                                                                                                                                                     ADDRESSEE:
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                                                                                                                        Illinois
                                                                                                                                                    6300 Sears Tower,
                                                                                                                                                                                                                  Bowie, Lemuel J.

NVENTION: Human `Thalassemia Mutations as a Predictor of WVENTION: Blood-Related Disorders
                                                                                                         United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (212)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
                                                                                                                                                                       Marshall,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      869-8864/9741
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                                                                                                                                                    , O'Toole,
fower, 233
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Pred. No. 3;
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                                                                                                                                                    Gerstein, Murray & Borun
South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 3;
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; LOCATION:
US-08-550-715-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Applicati
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 55; Conserv
TELEFAX: 301-208-6997 INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                              TELEPHONE: 301-527-2058
                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Glazer, Peter M.
TITLE OF INVENTION: TREATMENT OF HEMOGLOBINOPATHIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION: NAME: Gass, David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       601 TGGGCATAAAAGTCAGGGCAGAGCCATCTATTGCTTACA 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                            REFERENCE/DOCKET NUMBER:
                                                                                           NAME: Karta, Glenn E. REGISTRATION NUMBER:
                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                               CITY: Gaithersburg
                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 agggggaaggtccccggtccaggccagctgctgagtcca 99
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TELEFAX: 312/474-0448
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                                                                                                                                                                                                                                                                                                                                  20877
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                                                                                                                                                                                                                                                                                                                                                                                                200 Perry Parkway
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linear
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                                                                                          30,649
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Pred. No. 3.9;
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US-08-289-653-2/c

Sequence 2, Application US/08289653

Palent No. 5543322
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                                                                      INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1140 base pairs
TYPE: nucleic acid
STRANDENNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
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Best Local Similarity 55.6%;
Matches 55; Conservative
                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/887,284
FILING DATE: May 22, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
             FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                              ANTI-SENSE:
                                                             HYPOTHET ICAL:
                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Kazuaki KITANO et al.
TITLE OF INVENTION: DNA AND ITS USE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: HOMO Sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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 ORGANISM: Fusarium
                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 805 Fift
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 agggggaaggtccccggtccaggccagctgctgagtcca 99
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
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805 Fifteenth Street, N.W.,
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RESULT 12
US-08-289-653-1/c
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: PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-289-653-2
                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08289653 Patent No. 5543322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                         GENERAL INFORMATION: APPLICANT: Kazuak
                                     SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08,
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                              ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W.,
                                                                                                                                                                STREET: 805 Fiftee
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                        APPLICANT: Kazuaki KITANO et al.
TITLE OF INVENTION: DNA AND ITS
                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY:
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PUBLICATION INFORMATION:
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CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                                   COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                         124 CCTTGAGCTTGACAATGTACTTGCCAGCAATGGGCTGCGAACCACGAGCCTCGAGGAGAG 65
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                              FILING DATE:
                                                                                                                                           COUNTRY: U
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                      70 gtccccggtccaggccagctgctgag 95
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JOURNAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDENTIFICATION METHOD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANELLE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIBRARY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAPLOTYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49;
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                                                                                                                                                          U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                 Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26.5%;
                                          US/08/289,653
                                                                                                              5.25 inch, 500
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Pred. No. 12;
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RESULT 13
US-08-164-292B-15/c
; Sequence 15, Application US/08164292B
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; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-289-653-1
                                                                                                                                                                                        Matches
                                                                                                                                                                                                          Best
                                                                                                                                                                                                                    Query Match
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FILING DATE: May 22, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UNITS:
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OTHER INFORMATION:
PUBLICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                     605 GAGCGGGTTCCAGGACCGGGGCCGCG 580
                                                                                                                          665 CCTTGAGCTTGACAATGTACTTGCCAGCAATGGGCTGCGAACCACGAGCCTCGAGGAGAG 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POSITION IN GENOME: CHROMOSOME/SEGMENT: MAP POSITION:
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 2845 base pairs
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                                                                                      70 gtccccggtccaggccagctgctgag 95
                                                                                                                                          10 ccttgagatggacaaggcagaagtcggtggaggaaggggagccaccaggtcagggggaag 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MMEDIATE SOURCE:
                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                     DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Fusarium sp. STRAIN: S-19-5 (IFO 8884)
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STRANDEDNESS: doub
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                                                                                                                                                                                                    26.5%;
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Pred. No. 14;
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US-08-164-292B-17/c
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FILING DATE: 09-DEC-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GRACEY, NANCY J.
REGISTRATION NUMBER: 29,216
REFERENCE/DOCKET NUMBER: 2931
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 677-7000
TELEFAX: (415) 677-7522
TELEX: 34-0154
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 5100 base pairs
TPDE: nucleic acid
STEANNEYMERS: 40-0154
                                                                                                                                                                                              Sequence 17, Application US/08164292B Patent No. 5820868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 26.5%;
Best Local Similarity 61.4%;
Matches 43; Conservative
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                                                                                                                                                                       GENERAL INFORMATION:
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APPLICANT: MITTAL
                                             APPLICANT: MITTAL, SURESH K.
APPLICANT: GRAHAM, FRANK L.
APPLICANT: PREVEC, LUDVIK
APPLICANT: BABIUK, LORNE A.
TITLE OF INVENTION: RECOMBINANT PROTEIN PRODUCTION IN BOVINE
TITLE OF INVENTION: ADENOVIRUS EXPRESSION VECTOR SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: PREVEC, L
APPLICANT: BABIUK, L
TITLE OF INVENTION:
TITLE OF INVENTION:
                NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                    1682 GTCTTGAGGAGGACGGGAGGCACTCGGCGTGGGAACAGGAACAGCGGATGCTGCCGGAA 1623
                                                                                                                                                                                                                                                                                                                1622 GCTCCCTGGT 1613
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON
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    ADDRESSEE:
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LOCATION: 2..418
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STATE: California
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MORRISON & FOERSTER
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FRANK L.
LUDVIK
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RECOMBINANT PROTEIN PRODUCTION IN BOVINE ADENOVIRUS EXPRESSION VECTOR SYSTEM
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Pred. No. 16;
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STREET: 345 California Street CITY: San Francisco

California

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GENERAL INFORMATION:

APPLICANT: MITTAL, SURESH K.

APPLICANT: GRAHAM, FRANK L.

APPLICANT: PREVEC, LUDVIK

APPLICANT: BABIUK, LONG A

TITLE OF INVENTION: RECOMBINANT PROTEIN PRODUCTION IN BOVINE

TITLE OF INVENTION: ADEMOVIRUS EXPRESSION VECTOR SYSTEM

CORRESPONDENCES: 34

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 345 California Street

CITY: San Francisco

STATE: California
                                                                                                                                                                                                                                                                                                                                                                RESULT 15
US-08-164-292B-19/c
; Sequence 19, Application US/08164292B
harent No. 5820868
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NAME: GRACEY, NANCY J.

REGISTRATION NUMBER: 28,216
REFERENCE/DOCKET NUMBER: 29310-20021.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 677-700
TELEFAX: (415) 677-752
TELEY 34 0154
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 26.5%;
Best Local Similarity 61.4%;
Matches 43; Conservative
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1682 GTCTTGAGGAGGACGGGGAGGCACTCGGCGTGGGAACAGGAACAGCGGATGCTGCCGGAA 1623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1622 GCTCCCTGGT 1613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                    COUNTRY: USA
ZIP: 94104-2675
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LOCATION: 408..1331
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FILING DATE: 09-DEC-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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Pred. No. 16;
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Search completed: October Job time: 16974 sec
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ATTORNEY/AGENT INFORMATION:
NAME: GRACEY, NANCY J.
REGISTRATION NUMBER: 29,216
REFERENCE/DOCKET NUMBER: 2931
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 677-7900
TELEFAX: (415) 677-7522
TELEFAX: 44-0154
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                     Matches 43;
                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                   1682 GTCTTGAGGAGGACGGGGAGGCACTCGGCGTGGGAACAGGAACAGCGGATGCTGCCGGAA 1623
                                                                          1622 GCTCCCTGGT 1613
                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                              69 ggtccccggt 78
                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: 529..954
                                                                                                                                                     APPLICATION NUMBER: US/08/164,292B
FILING DATE: 09-DEC-1993
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nilarity 61.4%;
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Title:
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288.886 Million cell updates/sec
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Description
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                                 FEATURES
Source
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TITLE
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SOURCE
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Sequence 2 from Patent WO0177305.
AX281579
                                                      Andersson,L., Luthman,H. and Marklund,S.
Variants of the human amp-activated protein kinase gamma 3 subunit
Patent: WO 177305-A 2 18-OCT-2001;
                                                                                        Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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HSLB675

AC003677

AC003677

AC009017

AC076924

AC076924

AC0776924

AC0771896

AE071896

AE053985

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                       AX099776
Sequence 3
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            AX099776.1
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AX281582
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Mammalia; Eutheria;
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//db_xref="Ci:16608834"
//db_xref="Ci:16608834"
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DPAGVGTPPfCWDCLPSDCTASAAGSSTDDVELATEFPATEAWECELEGLLEERPALC
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LVANGVRAAPLWDSKKQSFVGMLTITDPILVLHRYXRSPLVQIYEEBQHKIETWREIY
LQGCFKPLVSISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHKRLKFLHIF
GSLLPRPSFLYRTIQDLGIGTFRDLAVVLETAPFLTALDIFYDBRVSALPVVNEGGQV
VGLYSRFDVJHLAAQGTYNLDMSVGEALRQRTLCLEGVLSGVPHESLGEVIDRIARE
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from Patent w00177305
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Patent WO0120003
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Sequence 29
AX099802
AX099802.1
                                                                                                                                  same, and uses thereof
Patent: WO 0120003-A 29 22-MAR-2001;
INSTITUT MATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA)
Andersson, Leif (SE) ; Looft, Christian (DE) ; Kalm,
Location/Qualifiers
                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
1 (Dases 1 to 2115)
Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A.,
Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy
                                                                                                                                                                                                                            Variants of the gamma chain of ampk, dna
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PATENT: WO 0120003-A 3 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA)
ANDRESSON, Leif (SE) ; Looft, Christian (DE) ; Kalm,
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Rogel-Gaillard,C., Iannuccelli,N., Gellin,
Chardon,P.
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Mammalia; Eutheria; Primates;
1 (bases 1 to 2109)
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                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
1. .1395
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29 from Patent W00120003
/protein_id="CAC35801.1"
/db_xref="GI:13538837"
                                               /note="unnamed protein product"
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YRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVVNECGQVVGLYSRFDVI
HLAAQQTYNHLDMSVCEALRQETLCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDE
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Pred. No. 1.4e-17;
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Gellin,J., le
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J., le Roy, P.
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Roy,P. and
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University of Agricultural Sciences, BMC box 597, Uppsala 751
                                                                                                                                                                                                                                                                                                                                                                                                                       Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A.,
Rogel-Gaillard,C., Paul,S., Gellin,J., Lundstrom,K.,
Kalm,E., Le Roy,P., Chardon,P. and Andersson,L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 2115)
Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M.,
Rogel-Gaillard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H.,
Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A mutation in PRKAG3 associated with excess glycogen content in pig
                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    skeletal muscle
Science 288 (5469), 1248-1251 (2000)
20280150
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                         /product-"AMP-activated protein kinase gamma subunit"
/protein_id="AAF73987.1"
/db_xref="GI:8215682"
/translation="MSFLEQENSSSWPSPAVTSSSERIRGKRRAKALRWTRQKSVEEG
                                                                                                           /gene="PRKAG3"
/note="AMPKG3"
                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
/map="2p"
                                                                                            /codon_start=1
                                                                                                                                                                    /gene="PRKAG3"
                                                                                                                                                                                             /tissue_type="skeletal muscle"
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                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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Pred. No. 1.4e-17;
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                                                                                                                                                                                                                                        RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Anderson, S., Baldwin, J., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Campopiano, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Graham, L., Grand, Grand-Pierre, N., Graham, L., Grand, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Kein, J., Larocque, K., Lanazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Menga, V., Morrow, J., O'Neil, D., Olivar, T.M., Oliver, J., Potterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Stange-Thomann, N., Stojanovic, N., Subramanian, K., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Direct Submission
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                                                                             Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 7, 2000 this sequence version replaced gi:7342115. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                         http://ftp.genome.washington.edu/RM/RepeatMasker.html
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1 (bases 1 to 152129)
Birren,B., Linton,L.,
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Center: Whitehead Institute/ MIT Center for Genome Research
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SSTDDVELATEFPATEAWECELEGLLEERPALCLSPQAPFPKLGWDDELRKPGAQIYM
RFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKKQSFVGMLTI
TDFILVLHRYYRSPLVQIYEIEQHKIETWREIYLQGCFKPLVSISPNDSLFEAYYTLI
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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Insert size: 149029; sum-of-contigs
Ouality coverage: 3.1 in Q20 bases;
Quality coverage: 3.3 in Q20 bases;
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Consensus quality: 135376 bases at least 040
Consensus quality: 143264 bases at least 030
Consensus quality: 146503 bases at least 020
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Contact: sequence_submissions@genome.wi.mit.edu
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46466 51285: contig of 4820 k
51286 51385: gap of 100 bp
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1006 1105: gap of 100 bp
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60595: contig of 4624 k
60695: gap of 100 bp
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16
201: gap of
7547: cc-
                      66595: contig of 10695: gap of 1173218: contig of 1
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466: gap of 100 bp
46365: contig of 3899 b
465: gap of 100 bp
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85123 93314: contig of 8192 bp in len
93315 93414: gap of 100 bp
93415 101193: contig of 7779 bp in len
101194 101293: gap of 100 bp
101294 113090: contig of 11797 bp in len
113091 113190: gap of 100 bp
113191 123496: contig of 10306 bp in len
123497 123596: gap of 100 bp
123597 137837: contig of 14241 bp in len
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137938 152129: cont
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77116 77215: gap of 100 bp
77216 85022: contig of 7807 bp in length
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85123 93314: contig of 8192 bp in length
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51386, .55871
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38280. 42366
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66696. .73218
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46466. .51285
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22029. .24319
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/db_xref="taxon:9606"
/clone="RP11-504G11"
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Sequencing vector: M13; 98%
Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 98% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0,990319
Consensus quality: 187795 bases at least 040
Consensus quality: 190513 bases at least 030
Consensus quality: 190513 bases at least 020
                                                                                                                                                 Consensus quality agarose-fp
Insert size: 200000; agarose-fp
Insert size: 194954; sum-of-contigs
Quality coverage: 5.58 in Q20 bases; agarose-fp
Quality coverage: 5.67 in Q20 bases; sum-of-contigs
Quality coverage: 5.67 in Q20 bases; sum-of-contigs
        * NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center project name: H_NH0647005
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On Feb 21, 2001 this sequence version replaced qi:8469048.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Washington University Genome Sequencing Center Center code: WUGSC
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Mammalia; Eutheria; Primates;
1 (bases 1 to 196554)
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AC073128.3 GI:13027579
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Homo sapiens chromosome 2 clone RP11-64705,
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93415. .101193
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85123. .93314
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101294. .113090
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44743 . 58275
/note="assembly_name:Contig27"
58376 . 73816
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92241. .113337
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113438. .130325
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73917. .92140
/note="assembly_name:Contig31"
|30426. .149287
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15884. .21906
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5204. .8524
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22007. .28887
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8625. .11856
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/db_xref="taxon:9606"
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VGLYSRFDVIHLAAQOTYNHLDMSVGEALRKRTLCLEGVLSCQPHESLGEVIDRIARE
QVHRLVLVDETQHLLGVVSLSDILQALVLSPAGIDPSGPEKI"
                                                                                 /translation="MEPGLEHALRRTPSWSSLGGSEHQEMSFLEQENSSSWPSPAYTS
SSERIRGKRRAKALRWTRQKSVEEGEPPGQGEGPRSRPAAESTGLEATFPKTTPLAQA
DPAGVGTPPTGHPCLPSDCTASAAGSSTDDVELATEFPATEAWECELEGLLEERPALC
LSPQAFFFKLGWDDELRKPGAQIYMRFEEHTCYDAWATSSKLVIFPDTWLEIKNAFFA
LVANGVBAAFLWDSKKOSFVGMLTITDFILVHRYYRSPLVQIVEIEQHKIETWREIT
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/protein_id="CAB65117.1"
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                                                                                                                                                                            Direct Submission
Submitted (03-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                                                                     Direct Submission
Submitted (08-NOV-2001) Genome
University School of Medicine,
MO 63108, USA
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University School of Med
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       Center: Washington University Genome Sequencing Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
Summary Statistics
Center project name:
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:

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VECTOR: DBACE3.6

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-1077K22; the clone sequenced to the right is RP11-64705. Actual start of this is at base position 1 of RP11-459119; actual end is at base position 206854 of RP11-459119.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               donor, as described by Oscegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
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Sus scrofa AMP-activated
                                                                        AF214520.1
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82; Conservative
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Mammalia; E
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Sus scrofa
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AX099774
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INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA)
INDERSON, Leif (SE); LOOft, Christian (DE); Kalm,
Location/Qualifiers
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                           scrofa
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                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="CAC35798.1"
/db_xref="GI:13538809"
/translation="mfffdeffcyDamATSSKLVIFDTMLEIKRAFFALVANGVRAAP
LMDSKKOSFVGMLTITDDFILVLHRYVRSPLVQIYEIEBHKIETWREIYLQGCFRPLVS
ISPNDSLFEAVYALIKNRIHRLEVLDPVSGAVLHILTHKRLLKFLHIFGTLLPRPSFL
YRTIQDLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVVNETGQVVGLYSRFDVI
HLAAQQTYNHLDMNVGGALRQRTLCLEGVLSCQPHETLGEVIDRIVREQVHRLVLVDE
TQHLLGVVSLSDILQALVLSPAGIDALGA"

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/db_xref="taxon:9823"
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                                                                        GI:8215683
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Sutheria; Cetartiodactyla; Suina; Suidae; Sus.
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from Patent W00120003.
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Pred. No. 8.2e-10;
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Best Local :
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                                     pig.
Sus scrofa
                                                                                 AX099800
Sequence 27 from Patent
AX099800
AX099800.1 GI:13538834
                    Eukaryota;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                          Similarity
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Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A.,
Rogel-Gaillard,C., Paul,S., Gellin,J., Lundstrom,K.,
Kalm,E., Le Roy,P., Chardon,P. and Andersson,L.
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1 (bases 1 to 1873)

Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M., Rogel-Gaillard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H., Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.
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580 c 535 g
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/product "AMP-activated protein kinase gamma subunit"
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1. .1873
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/db_xref="taxon:9823"
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1. .1873
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83.7%;
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Pred. No. 8.2e-10;
0; Mismatches 16;
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WO0120003.
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Euteleostomi;

PAT 02-APR-2001

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Gaps

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AUTHORS
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                                                                                                                        Variants of the gamma chain of ampk, dna same, and uses thereof Patent: WO 0120003-A 31 22-MAR-2001; INSTITUT NATIONAL DE LA RECHERCHE AGRONG Andersson, Leif (SE) : Looft, Christian Location/Qualifiers
                                                                                                                                                                                                                                                                                                                 pig.
Sus scrofa
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                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
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Sequence 31 from Patent
AX099804
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PATENT WO 0120003-A 27 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA)
ANDERSSON, Leif (SE); Looft, Christian (DE); Kalm,
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Rogel-Gaillard,C., Iannuccelli,N., Gellin,J.,
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Andersson, L., Looft,
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/db_xref="taxon:9823"
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/POOLEI__G=CAC35800.1"
/POOLEI__G=CAC35800.1"
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0; Mismatches 16;
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    6;
    Length 2022;
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Sus.
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                                                                                                                                        Ernst (DE)
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Matches 82; Conserv
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Submitted (10-DEC-1999) Dept Animal Breeding
University of Agricultural Sciences, BMC Box
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Rogel-Gaillard,C., Paul,S., Gellin,J., Lundstrom,K., Kalm,E., Le Roy,P., Chardon,P. and Andersson,L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 5888)
Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M., Rogel-Gaillard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H., Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          skeletal muscle
Science 288 (5469),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A mutation in PRKAG3 associated with excess glycogen content in pig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
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                                                                                /product="AMPK gamma subunit"
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HEMGEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLHDDSKKQSFYGMLTI
TDFILVLHRYVRSPLVQIYEIEEHKIETWREIYLQGGFKPLVSISPNDSTEFAVYALI
KNRIHRLPVLDPVSGAVLHILTHKRLLKFLHIFGTLLPRPSFLYRTIQDLGIGTFRDL
KNRIHRLPVLDPVSGAVLHILTHKRLLKFLHIFGTLLPRPSFLYRTIQDLGIGTFRDL
KNRIHRLPVLDPVSGAVLHILTHKRLLKFLHIFGTLLPRPSFLYRTIQDLGIGTFRDL
KNRIHRLPVLDPVSGAVLHILTHKRLKFLHIFGTLLPRPSFLYRTIQDLGIGTFRDL
KNRIHRLPVLDPVSGAVLHILDHVN
                                                                                                                                                                                                                                                                                                                                                                                                                 5294...5410)
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/codon_start=1
                                 GEALRQRTLCLEGVLSCQPHETLGEVIDRIVREQVHRLVLVDETQHLLGVVSLSDILQALVLSPAGIDALGA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="PRKAG3"
join(1. .154,515.
2771. .2825,3027.
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/product="AMPK gamma
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/db_xref="taxon:9823"
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1. .2825,3027. .3153,3286. .3451,4578.
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0; Mismatches 16;
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1339 t
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.4615,4791. .4937,
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Sus.
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AF336381/c
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                                                                                                                                  Ouery Match 71.7%; Score 72.4; DB 2; Length 227724; Best Local Similarity 83.7%; Pred. No. 5.8e-10; Matches 82; Conservative 0; Mismatches 16; Indels 0;
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source
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Submitted (17-JAN-2001) Genome Analysis, Institute of Molecular Blotechnology, Beutenberstr. 11, Jena 07745, Germany

NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus chromosome 1 clone PAC510; PAC457, *** PROGRESS ***, 3 unordered pieces.

AF336381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rump, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
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HTG; HTGS_PHASE1.
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17970
32747
32847
                                                                                                                                                                                                                                   Location/Qualifiers
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clone="PAC510; PAC457"
a 55423 c 56238 g 58199 t
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17969: gap of unknown length
32746: contig of 14777 bp in length
32846: gap of unknown length
227724: contig of 194878 bp in length.
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                                                                                                                                                                                                                                     201 others
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SEQUENCING IN
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Search completed: October 3, 2002, 14:49:54 Job time: 12114 sec

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              hits satisfying chosen parameters:
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          AAH4 3682
AAH4 3685
AAD03296
AAD033290
AAD03329
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AAS51418
AAS51418
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                                      PRKAG3 intron 2 -
PRKAG3 cDNA. Homo
Human AMPK gamma s
Human AMPK gamma sub
Pig AMPK gamma sub
Pig AMPK gamma sub
Sus scrofa PRKAG3
                                                                                                                                                                                                         Description
        DNA encoding
                       Pseudomonas aerugi
RESULT
AAH43682
ID AAH4
XX AAH4
XX AAH4
XX PRKA
XX Huma
XX Huma
KW meta
XX Homo
XX Homo
FH Key.
FT intr
FT
FT exon
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FT intr
FT
FT intr
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ALIGNMENTS

AAH43682 standard; DNA; 989

BP.

AAH43682; 21-JAN-2002

(first entry)
n 2 - intron 4.

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Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant; metabolic disease; diabetes; obesity; substitution; ds.
                         intron
                                                                                                                                                                                                                 Homo sapiens.
                                                                                               intron
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                       /number=
946..989
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/note= "3'
22..177
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178..541
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RESULT
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ID AAH4
XX AAH4
AC AAH4
AC AAH4
XX 11-C
XX Huma
KW Huma
KW meta
XX Homa
CX Homa
CX Homa
CX Homa
FH CDS
FT CDS
FT CDS
FT Vari
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Best Local :
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              variation
                                                                                          Homo
                                                                                                                metabolic disease;
                                                                                                         Human; AMP-activated protein kinase gamma 3 subunit; PRKAG3; variant; metabolic disease; diabetes; obesity; substitution; ss.
                                                                                                                                                     PRKAG3 cDNA
                                                                                                                                                                            21-JAN-2002
                                                                                                                                                                                                      AAH43685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequences given in AAH43681-84 represents genomic fragments encoding the human AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant is useful in determining a risk estimate of a metabolic disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New variants of human associated with a meta
                                                                                                                                                                                                                             AAH43685 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Fig 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
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                                                                                       sapiens
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            /product=
230
                                                 Location/Qualifiers
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                        "PRKAG3"
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Pred. No. 9.8
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             c;
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No. 9.8e-23;
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RESULT
AAD03296
ID AAD0
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AC AADC
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DE Huma
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Matches 101
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       Human AMPK gamma subunit muscle-specific isoform, PRKAG3 cDNA
                                      13-JUN-2001
                                                                 AAD03296
                                                                                          AAD03296
                                                                                                                                                                                                                                                                                                                                    Sequence 1647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 5; 25pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and for determining a risk estimate of diseases in subject by detecti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-APR-2000; 2000US-195665P
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                                                                                          standard;
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                                                                                       ВP
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Matches
                                                                 Query Match
Best Local
                                                                                                                                             useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3. Transgenic animal and host cell transformed with PRKAG3 or a heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.
                                                                                                                                                                                                                                                              evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are
                                                                                                                                                                                                                                                                                                        useful as therapeutic for treating carbohydrate metabolism disorders as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic
                                                                                                                                                                                                                                                                                                                                                                             The present sequence is a cDNA encoding human adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3. Mutation in prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is
                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of associated with energy metabolism such as diabetes, obesity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 12;
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Similarity 100.0%;
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diabetes; obesity; myopathy; cardiovascular disease; anorecti
testing; carbohydrate metabolism disorder; skeletal muscle;
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                                                Score 101; DB Pred. No. 1.1e-; Mismatches
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able to modulate AMPK activity

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CC (AMP) activated kinase (AMPK) gamma subunit muscle-specific isoform, CC complete PRKAG3. Mutation in Prkag3 results in an altered regulation of CC carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is CC useful as therapeutic for treating carbohydrate metabolism disorders such CC as diabetes, obesity, and disorders associated with muscle metabolism Such as myopathy and cardiovascular diseases, to modulate AMPK CC activity, and for restoring a normal AMPK function. PRKAG3 sequence CC and its functionally altered mutants are useful for the diagnostic CC evaluation, genetic testing and prognosis of a metabolic disorder, CC preferably a carbohydrate metabolism disorder. Primers that can detect CC a genetic polymorphic marker linked to a sequence encoding PRKAG3, are CC useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3 or a consisting of PRKAG3 or its mutant, are useful for screening campands while to modulate a marker that the consisting of PRKAG3 or its mutant, are useful for screening campands while to modulate a marker of the consisting of prkAG3 or its mutant, are useful for screening campands while to modulate a marker of the consisting of prkAG3 or its mutant, are useful for screening campands while to modulate a marker of the consisting of prkAG3 or its mutant, are useful for screening campands while to modulate a marker of the consisting of prkAG3 or its mutant, are useful for screening campands while to modulate a marker of the consisting of prkAG3 or its mutant, are useful for screening campands while to modulate a marker of the consisting of prkAG3 or its mutant, are useful for screening campands while to modulate a marker of the consisting of prkAG3 or its mutant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) ANDERSSON L.
) LOOFT C.
) KALM E.
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                                                                                                                                                                                                                      Looft C,
Gellin
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472..1389
/*tag= b
/product= *
1390..1867
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⇒ Roy •
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Pred. No. 1.1e-22;
Pred. No. 1.1e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      scrofa PRKAG3 protein"
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                                                                                                                                                                                                                    Chardon
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                                                                                                                                                                                                             Robic don P;
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                                                                                                                                                                                                                                     Rogel-Gaillard
                                                        disorders and
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is a cDNA encoding pig adenosine monophosphate CC (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, CC PRKAG3. Prkag3 gene is located in the RN locus of chromosome 15.

CC Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as CC diabetes, obesity, and disorders associated with muscle metabolism cs. Such as myopathy and cardiovascular diseases, to modulate AMPK CC and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, CC are ferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3. are CC useful for detecting a dysfunction of carbohydrate metabolism for carbohydrate metabolism of a functionally altered allele of PRKAG3. CC Transgenic animal and host cell transformed with PRKAG3 or a heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid can a sequence encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                10-SEP-1999;
18-MAY-2000;
(INRG ) INRA INST NAT RECH AGRONOMIQUE. (ANDE/) ANDERSSON L.
                                                                                                11-SEP-2000;
                                                                                                                                   22-MAR-2001
                                                                                                                                                                WO200120003-A2
                                                                                                                                                                                                                                                                                Sus scrofa
                                                                                                                                                                                                                                                                                                               chromosome
                                                                                                                                                                                                                                                                                                                           PKRAG3; dlabetes; obesity; myopathy; cardiovascular disease; anorec genetic testing; carbohydrate metabolism disorder; skeletal muscle; cystathione beta synthase; CBS; cardiant; gene therapy; RN locus;
                                                                                                                                                                                                                                                                                                                                                   Pig: gamma subunit; adenosine monophosphate-activated kinase; AMPK; PRKAG3; diabetes; obesit; myopathy; cardiovascular disease; anorec
                                                                                                                                                                                                                                                                                                                                                                                                  Pig AMPK gamma subunit muscle-specific isoform, complete PRKAG3 CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                             13-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  403 tccccagaggtgctgttacccaggctgggctgggatgatgagctgcagaagccgggggcc 462
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                                                                                                                                                                                                                                                                                                               15; ss.
                                                                                                                                                                                                                                                                                                                          beta synthase;
                                                99EP-0402236,
2000EP-0401388
                                                                                                2000WO-EP09896
                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP; 380 A; 583 C; 529 G; 375 T; 0 other;
                                                                                                                                                                                                                              Location/Qualifiers
1..1395
                                                                                                                                                                                               /product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA; 1873
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83.7%;
                                                                                                                                                                                          "Sus scrofa complete Prkag3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 72.4; DB 22
Pred. No. 1.3e-13;
0; Mismatches 16
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                                                                                                                                                                                                                                                                                                                      cardiant; gene
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                                                                                                                                                                                                                                                                                                                      therapy; RN locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1867;
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                                                                                                                                                                                        protein.
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                                                                                                                                                                                                                                                                                                                                                     anorectic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
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                                                                        PRKAG3; diabetes;
genetic testing; c
cvstathione beta (
                                                                                                                        Pig;
                                                                                                                                                                                 13-JUN-2001
                                                                                                                                                                                                               AAD03321;
                                                                                                                                                    Sus scrofa
                                                                                                                                                                                                                                            AAD03321 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1873
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                associated with energy metabolism such as diabetes, obesity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New variants of the gamma subunit of vertebrate adenosine monophosphate activated kinase for diagnosis or treatment of disorders
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Iannuccelli N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (KALM/) KALM E.
                                                                                                                                                                                                                                                                                                                      469
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                                                                        gamma subunit; adenosine monophosphate-activated kinase; AMPK; G3; diabetes; obesity; myopathy; cardiovascular disease; anorectic; tic testing; carbohydrate metabolism disorder; skeletal muscle; athione beta synthase; CBS; cardiant; gene therapy; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 62-64;
                                                                                                                                                   PRKAG3 splice variant DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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N, Gellin
                                                                                                                                                                               (first entry)
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Location/Qualifiers
1..1545
                                                                                                                                                                                                                                            DNA;
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83.7%;
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   535 G; 376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 72.4;
No. 1.
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Chardon P;
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1.3e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           16;
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64 cagatctacatgcgcttcatgcaggagcacacctgcta 101

caggictacatgcacticatgcaggagcacacctgcta

656

4 tccccgcaggccccatttcccaagctgggctgggatgacgaactgcgggaaaccccggcgcc 63

tccccagaggtgctgttacccaggctgggctgggatgatgagctgcagaagccgggggcc 618

559

Matches

Conservative

0;

Mismatches

16;

Indels

0;

Gaps

0;

Pred. No. 1

.3e-13

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619

AAS51418

AAS51418

standard;

DNA; 1428

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CC kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3 splice of contraint DNA. Prkag3 gene is located in the RN locus of chromosome 15. CC Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as CC therapeutic for treating carbohydrate metabolism disorders such as CC diabetes, obesity, and disorders associated with muscle metabolism CC such as myopathy and cardiovascular diseases, to modulate AMPK CC activity, and for restoring a normal AMPK function. PRKAG3 sequence CC and its functionally altered mutants are useful for the diagnostic cc evaluation, genetic testing and prognosis of a metabolic disorder, CC preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3 are cuseful for detecting a dysfunction of carbohydrate metabolism resulting CC from the expression of a functionally altered allele of PRKAG3. are CC from the expression of a functionally altered allele of PRKAG3 are CC from the expression of a functionally altered allele of PRKAG3. CC from the expression of a functionally altered allele of PRKAG3 or a metabolism resulting CC form the expression of a functionally altered allele of PRKAG3 or a metabolism resulting CC functional practice and host cell transformed with PRKAG3 or a sequence encoding the for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                         Sequence 2022 BP; 412 A; 623 C; 593 G; 394 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is pig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 12; Page 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        myopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Andersson L,
Iannuccelli N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-SEP-2000; 2000WO-EP09896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB;
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(ANDE/)
(LOOF/)
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18-MAY-2000; 2000EP-0401388
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, Gellin
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/product= "Sus scrofa Prkag3 splice variant"
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71.78;
83.78;
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-⊶ Roy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           adenosine monophosphate (AMP)-activated muscle-specific isoform, PRKAG3 splice
                 Score 72.4;
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                 DB
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                 22;
               Length
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                 2022;
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The invention relates to antisense inhibitors of genes essential to CC prokaryotic cellular proliferation, their use in identifying the CC genes, their use in the discovery of novel antibiotics, the essential CC genes themselves and the encoded proteins. The prokaryotes used are CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella CP pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The CC invention is also useful for the identification of potential new targets CC for antibiotic development. The antisense nucleic acids can also be used CC indentify proteins used in proliferation, to express these proteins. CC and to obtain antibodies capable of binding to the expressed proteins. CC The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen CC for homologous nucleic acids which are required for cell proliferation in CC a wide variety of organisms. The present sequence encodes an CC essential prokaryotic cellular proliferation protein.

CC Note: The sequence data for this pattent did not form part of the printed specification, but was obtained in electronic from wire only hombicable.
                                                                                                                               Matches
                                                                1218
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23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
                                                                                                                                                                                                          Sequence 1428 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids {\bf r}
                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haselbeck R,
Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas aeruginosa
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22 - DEC - 2000;
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                                 63
                                                                          3 gtccccgcaggccccatttcccaagctgggctgggatgacgaactgcgggaaacccggcgc 62
                                                                                                                                            Local Similarity
gctgagcatcatgctgatcatgccggagcac 1308
                ccagatctacatgcgcttcatgcaggagcac 93
                                                        gttccgtatgtggctatatccctggctgacctgggcggtgatcctgttcatcgtcgccgc 1277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-611495/70
                                                                                                                               53;
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                                                                                                                             Conservative
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2000US-206848P.
2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
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Xu HH;
                                                                                                                                                                                                       206 A; 525
                                                                                                                                        29.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zyskind
                                                                                                                     Score 30.2; DE Pred. No. 3.2; 0; Mismatches
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                                                                                                                           0,
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                                                                                                                                                                                                       C; 423
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                                                                                                                                                                                                      <u>ი</u>
                                                                                                                                                                                                      274 T; 0 other
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                                                                                                                                                         DВ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Trawick JD,
                                                                                                                                                    Length 1428;
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64 cagatetacatgegetteatgeaggageacacetg

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CC Note: The sequence data for this patent did not appear in the printed content of the sequence of the invention.

CC at ftp.wipo.int/pub/published_pct_sequences.
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AAS74198
                                                                                           Ouery Match
Best Local Similarity
                                                                              Matches
          2710
                                                                                                                                                             Sequence 3918 BP; 1328 A; 872 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID No 10002; 103pp; English
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23-AUG-2000; 2000US-0649167
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tccccttatcccccatcctccctgctgaggtgtgtgggcgcacagcgcggggactggcggg 2769
                 tccccgcaggccccatttcccaagctgggctgggatgacgaactgcggaaacccggcgcc 63
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                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human diagnostic protein #10002
                                                                                         29.1%;
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                                                                       Score 29.4; DB Pred. No. 6.9; 0; Mismatches
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                                                                                                                                                             822 G;
                                                                                                                                                             896 T; 0 other;
                                                                                                           DB
                                                                         41;
                                                                                                         23;
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                                                                     Gaps
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2770 cagctccacctgcagccccagtgcgagatccactg 2804

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В
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AAS80424
                                                                              Matches
                                                                                         Query Match
Best Local Similarity
2710 teceettateeeceateeteeetgetgaggtgtgtgggegeaeagegegggaetggeggg 2769
                                                                                                                                                    Sequence 3918 BP; 1328 A; 872 C; 822 G; 896 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutatio responsible for genetic disorders or other traits and to assess
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23-AUG-2000;
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                    4 teccegeaggececattteceaagetgggetgggatgaegaaetgeggaaaeceeggegec 63
                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences.
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                                                                                       29.1%;
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                                                                     Score 29.4; DB Pred. No. 6.9; 0; Mismatches
                                                                         0;
                                                                                                     DB 23;
                                                                     41;
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                                                                                                   Length
                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful in of mutations
                                                                                                     3918;
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Query Match Best Local S Matches 54

Local Similarity

29.1%; 56.8%;

Score 29.4; Pred. No. 7; Mismatches

DB 23;

41;

Indels Length 4397;

0

Gaps

0,

976 T; 0

other;

Conservative

0;

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, compolypeptide (II) sequences. (I) is useful as hybridisation probes, compolypeptide (II) sequences, oligomers, and for chromosome compolypeptide are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques compolypeptide in tissue, as molecular weight markers and as expressed sequence tags (II). (II) is useful for generating antibodies against it, detecting or compolypeptide in tissue, as molecular weight markers and as imaging of sites expressing (II). (I) and (II) are useful in medical compolypeptide and polypuncleotide sequences have applications in composition of sites expressing (II). (I) and (II) are useful for treating composities, forensis, gene mapping, identification of mutations composities, forensis, gene mapping, identification of mutations composities for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and composities coding sequences and products dependent on DNA and composities and polypeptide and products dependent on the printed specification, but was obtained in electronic format directly from WIPO at final interval and produce format directly from WIPO at final interval and produce format directly from WIPO at final interval and produce format directly from WIPO at final interval and produce format directly from WIPO at final interval and produce format directly from WIPO at final interval and produce format directly from WIPO at final interval and produce format directly from WIPO at final interval and produce format directly from WIPO at final and pr
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AAS74446
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          Sequence 4397
                                                 at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide and encoded polypeptides, us diagnostics, forensics, gene mapping, identification of responsible for genetic disorders or other traits and to responsible for genetic disorders or other traits.
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23-AUG-2000;
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BP; 1506 A; 980 C; 935 G;
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2000US-0649167.
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The invention relates to isolated polynucleotide (I) and CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC control of (II) are to treat disease states involving CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as is a cod supplement. (II) and its binding partners are useful in medical classing of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. CC diagnostics, forensics, gene mapping, identification of mutations in CC diagnostics, forensics, gene mapping, identification of mutations cc responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences. AAS64197-AAS94564 represent novel human CC diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed captification, but was obtained in electronic format directly from WIPO
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AAS73340
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Sequence 5122 BP; 1815 A; 1151 C; 1032
                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID No 9144; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
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23-AUG-2000; 2000US-0649167
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                               ftp.wipo.int/pub/published_pct_sequences.
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                                                     Query Match
Best Local Similarity
Matches 38; Conserv
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                                                                                                                                                                                       capable of detection 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                     Sequence 1406
                                                                                                                                                      The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection
                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 9988; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-656860/75.
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11-JUL-2000;
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(ABB57737-ABB72072)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila; developmental biology; cell signalling;
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                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences.
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                                                       Conservative
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2000US-0614150
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                                                                                                                  BP; 358 A; 409 C; 404 G; 235 T; 0 other;
                                                                 28.7%;
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Pred. No. 7
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Best Local :
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                                                  Drosophila melanogaster genomic polynucleotide SEQ ID NO 9979.
Drosophila melanogaster
                                    Drosophila;
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                        pharmaceutical;
                                                                                 26-MAR-2002
                                                                                                                            ABL19502 standard;
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                                                                                                                                                                                                                                                                                                            The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                              Sequence 3406
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 9985; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Venter JC, Adams M,
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11-JUL-2000;
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                                                                                                                                                                                                                                     38;
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                  developmental biology; cell signalling; insecticide;
cal; gene; ds.
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                                                                              (first entry)
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2000US-0614150
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71.7%;
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Pred. No. 9;
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Search completed: October Job time: 14316 sec
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                                                            3377 ctgaagcccggcgcccggctgtgcccgcgctgctttcaggagctctccgacta 3429
                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosphila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL0176-ABL30511), expressed DNA sequences (ABL01840-ABL6175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                               Sequence 3593 BP;
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                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 9979; 21pp + Sequence Listing; English.
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11-JUL-2000; 2000US-0614150
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                                                                           49 cggaaacccggcgcccagatctacatgcgcttcatgcaggagcacacctgcta
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                                                                                                                                       Similarity
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      BB630381 BB830381
A1106144 db03d12_p
BE540087 601060879
B1199916 602760950
BH140228 ZMMBBb000
ALL50666 Anopheles
ALZ12510 Tetraodon
BM133818 NXLV_012
BE269692 601185836
BE269692 601185836
BG394974 602457369
BM468546 ACENCOURT
AAZ64931 LD08544.5
T95291 ye43b03.s1
AA246471 LD05631.5
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BI775360 467815 MA
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802	592	525	517	812	712	260	904	742	718	707	605	593	591	509	448	445	339	750	569	738	666	629	627	589	583	561	554
12	12	9	9	9	φ	9	10	10	9	12	φ	12	9	10	9	10	10	10	10	9	10	9	10	9	10	10	9
вн077939	AZ870322	AA922163	AW631272	AA519383	BB623242	AW816448	BF033403	v	AV753229	AG130442	AA195150	вн140663	AW678584	BG560394	AW497449	BG558441	BF773519	BM019844	BG414376	AI544103	BI242279	A1259247	B1633071	AA539970	BI232284	BI229683	AI260567
BH077939 RPCI-24-2	2M0182F	AA922163 om42b02.s	1h80f03.	AA519383 TgESTzz54	BB623242 BB623242	AW816448 QV4-ST023	BF033403 601457923	BE394076 601312450	AV753229 AV753229		AA195150 zr34c12.r	вн140663 гммввь000	AW678584 WS1_16_E0	BG560394 RHIZ2_73_	AW497449 660052B03	BC558441 RHI22_67_	CM2-1T00	BM019844 603648189	76 HVSMEkO	LD46336.5	2279 RE39577	LP02620.5	1 SD2704	LD19281.	4 RE283	83 RE27	AI260567 LP04480.5

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JOURNAL MEDLINE COMMENT RESULT 1 BF890374 LOCUS DEFINITION REFERENCE AUTHORS SOURCE ORGANISM ACCESSION VERSION FEATURES KEYWORDS TITLE source Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001) 21180013 Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Email: smith@email.marc.usda.gov Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G. Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and BF890374 444 bp mrNA linear 291826 MARC 3BOV Bos taurus cDNA 5', mRNA sequence. BF890374 BF890374.1 GI:12281760 EST. FORMARD: AGGAAACAGCTATGACCAT BACKMARD: GTTTCCCACTCACCACG BALE: 57 row: H column: 11 Seq primer: ATTTAGGTGACACTATAG PCR PRimers Tel: 402 762 4366 Fax: 402 762 4390 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Keele, J.W. Bovidae; Bovinae; Bos. Bos taurus (bases 1 to 444) -minmatch 12 options. /organism="Bos taurus" /db_xref="taxon:9913" Location/Qualifiers EST 25-APR-2001

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RESULT
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467815 MA
                                                                                                                                                                                                                                                                                                                                                                                      Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore minmatch 12 options.
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                /tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6: Site_1: XbaI; inches"vector: pCMV SPORT6: Site_1: XbaI; inches"vector: pCMV SPORT6: Site_1: XbaI; inches" made from pooled tissue from testi: Library made from pooled tissue from testi: Semitendonosus muscle, longissimus muscle, and endometrium. "
173 c 163 g 93 t
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147 c 139 g 67 t
                                                                                                                                                                 /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
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/tissue_type="pooled"
/lab_host="DH10B"
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Pred. No. 7.5e-11;
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rom pooled tissue from testis, thymus,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: genome-res@gsc.riken.go.jp,
URU:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1650 (2000)
wagi,K., Pujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
hayashizaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
hayashizaki,Y., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizaw,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute Opposized and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jar
Tel: 81-45-503-9222
Fax: 81-45-503-9216
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83; Conserv
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Unpublished (2001)
Contact: Yoshihide Hayashizaki
                                                                           Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
                          further details.
e mouse tissues.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCCCCACAGGCCCCACTTCTTGGCCTGAGTTGGGATGACCAACTTCACAAACCCGGAGCC 555
                                                  Email: fishman@ngh.cvrc.harvard.edu
http://zebrafish.mgh.harvard.edu
The original clones used for sequencing are no longer available;
the library is available from Mark C. Fishman.
                                                                                                                                              Contect: Mark C. Fishman
Cardiovascular Research Center
Massachusetts General Hospital
Mail code 1494100A, 149 13th Street,
                                                                                                                                                                                                                 Expressed Sequences from The Adult Zebrafish Heart Unpublished (1998)
                                                                                                                                                                                                                                                              Chen, J.N., DeSauvage, F., Hosobuchi, M., Jackson, D.G. and Fishman
                            the library is available
Insert Length: 326 Std
Seq primer: pl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Site_1: SalI; Site_2: BamHI; cDNA library
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/lab_host="DH10B"
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/db_xref="taxon:10090"
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Pred. No. 1.7e-09;
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Query Match Best Local : Matches

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30.3%;

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679; 0

Mismatches

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                                                                                                                                                                                                  High quality sequence stop: 668
Location/Qualifiers
                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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             124
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   /note-*Organ: cervix; Vector: pcMV-SPORT6; Site_1: Not1; Site_2: Sali; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5 kb. Library prepared by Life Technologies.*

1 226 c 177 g 152 t
                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                      /clone_lib="NIH_MGC_10"
/cell_line="MGC36"
                                                                                                                                    /clone="IMAGE:3447378"
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/lab_host="E. coli XL1 Blue"
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/clone_lib="ZF adult heart library"
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/strain="AB"
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Pred. No. 34;
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Plate: LLCM1783 row: c column: 13
High quality sequence start: 5
High quality sequence stop: 669.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC
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NIH-MGC http://mgc.nci.nih.gov/
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BI199916
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Unpublished (1999)
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216 c
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/lab_host="DH10B (phage-resistant)"
/note="organ: brain; Vector: pOTB7; Site_1: xhoI; Site_2:
ECORI; cDNA made by Oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_"IMAGE: 4896324"
/clone_lib="NIH_MGC_19"
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/db_xref="taxon:9606"
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67.28;
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                                                                                                                                                                                                 Score 30.4; E
Pred. No. 78;
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                                                          Anopheles gambiae
Eukaryota; Metazo
Pterygota; Neopte
                                                                                                                                                                                 CNS01MA1 894 bp DNA linear GSS 14-JUN-2001 Anopheles gambiae GSS SP6 end of clone 21E19 of NotreDame1 library from strain PEST of Anopheles gambiae (African malaria mosquito),
                                                                                                                                                                                                                                                                                                                                                                                                                                  47;
              Genoscope
                                            Culicoidea;
                                                                                                      African malaria mosquito.
                                                                                                                                        AL150666.1 GI:7011145
                                                                                                                                                                    genomic survey sequence.
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Zea mays
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Clemson University
100 Jordan Hall, Clemson, SC 29634, U
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High quality sequence stop: 510
Location/Qualifiers
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Class: BAC ends
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47; Conservative
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/strain="B73"
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/clone_lib="Maize B73"
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                                                        Neoptera; Endopterygota; Diptera; Nematocera;
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                                                                       Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at
                                                                                                                                                                                                                                                                                                                                                                        Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii, Meopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
                                                                                                                                                                            Roest Crollius, H., Jaillon, O., Dasilva, C., Boune Bernot, A., Fizames, C., Wincker, P., Brottier, P., Saurin, W. and Weissenbach, J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AL212510.1 GI:7871329
GSS; genome survey sequence.
Tetraodon nigroviridis.
                                                                              Direct Submission
                                                                                                                                   Unpublished
                                                                                                                                                    Tetraodon nigroviridis
                                                                                                                                                                       Human gene number estimate
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Billault,A., Quetier,F., Sauri
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Tetraodon nigroviridis genome survey sequence T7 end of clone
163G17 of library G from Tetraodon nigroviridis, genomic survey
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Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue d
Roux, Paris 75015, France
This clone is from an A. gambiae BAC library provided by
Collins and sequenced by Genoscope in collaboration with
Laboratory of Biochem. and Biol. Molec. of Insects, Insti
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Roth,C.W., Brey,P.T., Ke,Z., Collins,F.H. and Weissenbach,J.
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191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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/note="end : SP6"
256 c 234 g 2:
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/clone="21E19"
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Saurin,W., Bernot,A. and
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                                                                                                                                                              Direct Submission
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ dat
This sequence is a single read and was generated as
scale clone-end sequencing project of the Tetraodon
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                        Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottler, P., Quetier, F., Saurin, W. and Weissenbach, J.
Human gene number estimate provided by genome wide analysis using Tetracdon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                            Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi, Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
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Tetraodon nigroviridis genome survey sequence T7 end of clone
005N22 of library G from Tetraodon nigroviridis, genomic survey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
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    /Organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/db_xref="105N22"
/clone=105-N2"
/clone_lib="G"
/note="Genoscope sequence ID : COBG005DG11xD1-end :
1 313 c 312 g 210 t 1 others
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/db_xref="taxon:99883"
/clone="163G17"
/clone_lib="G"
/note="Genoscope sequence ID : COA
1 263 c 305 g 160 t 3
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       BE269692 930 bp
601185836F1 NIH_MGC_8 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           North Carolina State University Tel: 919 515 7800 Fax: 919 515 7801 Email: ajohnson@unity.ncsu.edu Seq primer: T3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
Contact: Johnson, Arthur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; 1 (bases 1 to 655)
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BM133818 BM133818 GI:17141057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="NXLY_012_F09"
/clone_lib="NXLV (Nsf Xylem Late wood Vertical)"
/tissue_type="primary xylem"
/dev_stage="late wood"
/lab_host="XL1-Blue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain∾"Coastal plain loblolly pine from North Carolina"
/db_xref="taxon:3352"
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Pred. No. 1.3e+02;
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Pred. No. 1.3e+02;
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Pinus; Pinus.
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                 Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih
                                              NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae 1 (bases 1 to 955)
                                                                                                                                                  Homo sapiens
                                                                                                                                                                                          EST
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BG394974
BG394974.1 GI:13288422
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602457369F1 NIH_MGC_16 Homo sapiens
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Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.
plate: LLCM237 row: g column: 09
High quality sequence stop: 238.
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Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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//lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="organ: lymph; Vector: pOTB7; Site_1: xhoI; Site_2: EccRI; cDNA made by oligo-dT priming. Directionally cloned into EccRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
a 228 c 267 g 209 t
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/clone_lib="NIH_MGC_8"
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/db_xref="taxon:9606"
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Pred. No. 1.4e+02;
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BM468546
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Best Local Similarity
Matches 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              896 CAC 898
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33 ctgggatgacgactgcggaaacccggcgcccagatctacatgcgcttcatgcaggagca 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cac 95
                                                                                                                                                                             cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov now: m column: 09 High quality sequence stop: 725.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGENCOURT_6475521 NIH_MGC_72
5', mRNA SECTION OF THE MINISTRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plate: LLCM1297 row: j column: 17 High quality sequence stop: 717.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
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/clone_lib="NIH_MCC_16"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/lab_host="Phage-resistant)
/lab_host="Phage-resistant"
/lab_host="Phage-resistan
                                                                    /organism="Homo sapiens"
/clone="IMAGE:5578160"
                                    /db_xref="taxon:9606"
                                                                                                                                             Location/Qualifiers
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/db_xref="taxon:9606"
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Pred. No. 1.6e+02;
""smatches 21;
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Best Query Match

Local Similarity

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Score 29; 1 Pred. No. 1.

DB 9; .6e+02; es 15;

Length 313;

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                                                                                                                                                                                                                                                                                                                               Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Blast expect value = 1.1E-117 on x03121: Drosophila melanogaster
serendipity (sry) locus DNA sequence
Plate: 85 row: D column: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harvey,D., Brokstein,P., Hong,L.,
Lewis,S. and Rubin,G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 313)
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LD08544.5prime LD Drosophila
Drosophila melanogaster cDNA
AA264931
                                                                                                                                                                                                                                                                                                              Plate: 85 row: D column: 8
High quality sequence stop: ?
                                                                                                                                                                                                                                                                                                                                                                                                                        BDGP
Lawrence Berkeley National Lab
Berkeley, CA 94720, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Stapleton, M.
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Similarity 64.2%;
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          72
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/note=*Organ: embryo; Vector: BlueScript SK; Site_1: EcoRI
; Site_2: XhoI; Constructed using Stratagene ZAP-cDNA
Synthesis klt. Oligo dT-primed and directionally cloned at
EcoRI and XhoI in BlueScript SK(+/-)*
                                                                                                      /clone_lib="LD Drosophila melanogaster embryo BlueScript"
/sex="male and female"
/dev_stage="0 to 24 hours mixed stage embryonic"
/lab_host="SOLR"
                                                                                                                                                                                       /organism="Drosophila melanogaster"
/db_xref="BBGP_EST:BDC1n007879"
/db_xref="taxon:7227"
/clone="LD08544"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pcMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies "
244 c 303 g 174 t 3 others
                                                                                                                                                                                                                                                                                           Location/Qualifiers
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Pred. No. 1.9e+02;
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2000 Compugen
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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TELEPHONE: 317-276-3885
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27484 CCGCTGCTGGGCAGCGGCGTCGAACTGCCGGAGTCCGGTGACCGGATGTACA 27535
                                                                    NAME/KEY:
LOCATION:
FEATURE:
                                                                                                            LOCATION: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: PAUL R. CANTRELL. 11
STREET: LILLY CORPORATE CENTER
                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: Macintosh 7.0 SOFTWARE: Microsoft Word 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Rao, Nagaraja R.
APPLICANT: Richardson, Mark A.
APPLICANT: Rosteck, Paul R., Jr.
TITLE OF INVENTION: PLATENOLIDE SYNTHASE GENE
                                                                                                                                                      LOCATION: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CANTRELL, PAUL R.
                             FEATURE:
                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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NAME/KEY:
NAME/KEY:
LOCATION:
                                        NAME/KEY:
                                                                                                                                                                                                                                     LENGTH: 44377 base pairs
TYPE: nucleic acid
STRANGENESS: single
                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/804,198 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: INDIANAPOLIS STATE: IN
                                                                                                                                          NAME/KEY:
                                                                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 cccaagctgggctgggatgacgaactgcggaaacccggcgcccagatctaca 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
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Rao, Nagaraja R.
Richardson "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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                                                                                                                        CDS
14046..20036
CDS
36155..41830
                                        CDS
31329..36071
                                                                                CDS
20110..31284
                                                                                                                                                                    CDS
350..14002
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36155..41830
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31329..36071
                                                                                                                                                                                                            DNA (genomic)
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Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 2113570 cccgcacgcgtggatccgcaacccggttacggctgacgagatctggcagcccggcccaca 2113629
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APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 198-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-103-840A-2
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                                                                                                                                                                                                                                                                                                            Sequence 17, Appli Patent No. 6214358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 47; Conserv
                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Singh, Mohan Bir;
APPLICANT: Smith, Penelope; and
APPLICANT: Knox, Robert Bruce
TITLE OF INVENTION: Protein Allergens
TITLE OF INVENTION: Dactylon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09103840A Patent No. 6294328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                          NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                              STALL.
COUNTRY: UL-
COUNTRY: UL-
                                                                                                          CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 gatctacatgcgcttcatgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 cccaagctgggctgggatgacgaactgcggaaaacccggcgcccagatctaca
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                                                                                                                                                                                                                                                                                                                                                                                                             gaaccggatggtcagctggc 2113649
                                                                                           Massachusetts
                                                                                                                                                                                                                                                                                                                           Application US/08441507
                                                                                                                           28 State Street
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Pred. No. 40;
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Pred. No. 17
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                                                                                                                                                                                                                  of the
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                                                                                                                                                                                                                  Species
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CURRENT APPLICATION DATA:

US/08/441,507

OPERATING SYSTEM: PC SOFTWARE: ASCII text

PC-DOS/MS-DOS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCEX/DOCKET NUMBER: IMI-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                          SEQ ID NO 4
LENGTH: 6085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/09029603 Patent No. 6210935
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                APPLICANT: Pospiech, Andreas
TITLE OF INVENTION: Staurosporin Biosynthesis Gene Clusters
FILE REFERENCE: 4-2055/A/PCT
CURRENT APPLICATION NUMBER: US/09/029,603
CURRENT FILING DATE: 1998-03-20
EARLIER APPLICATION NUMBER: PCT/EP96/03643
EARLIER FILING DATE: 1996-08-19
NUMBER: OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Schupp, Thomas
APPLICANT: Engel, Natalie
APPLICANT: Bietenhader, Jurg
APPLICANT: Toupet, Christine
                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. 2.0
                                                                 NAME/KEY: misc_RNA
LOCATION: (1747)..(2553)
OTHER INFORMATION: ORF
                                                                                                                                                                                                   TYPE: DNA ORGANISM: Streptomyces longisporoflavus FEATURE:
LOCATION: (2593)..(4011)
OTHER INFORMATION: ORF
                 NAME/KEY: misc_RNA
LOCATION: (2593)...
                                                     FEATURE:
                                                                                                                                              NAME/KEY: misc_RNA
LOCATION: (378)..(1665)
OTHER INFORMATION: ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 07/969,875
FILING DATE: 30-October-1992
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras Amu "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 594 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/0 FILING DATE: 15-May-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 cgcaggccccatttcccaagctgggctgggatgacgaactgcggaaaccccggcgcccaga 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGTTCGGCGCCATGGCCAAGAAGGGCGAGGAGGACAAGCTGCGCAAGGCCGGCGAGCTGA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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US-08-463-081B-13/c

Sequence 13, Application US/08463081B

; Patent No. 5871960

; Patent No. 5871960 5837487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNIN.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
TOWNITER: THE PC-DOS/MS-DOS
TOWNITER: THE PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 25.5%;
Best Local Similarity 56.5%;
Matches 48; Conservative
                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/463,081B
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 08/104,736
FILING DATE: 10-AUG-1993
PRIOR APPLICATION UNBER: US 07/796,066
FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: VIVIANA AMZEI, Ph. D.
REGISTRATION NUMBER: 30,930
REGISTRATION NUMBER: 966 38150
REFERENCE/DOCKET NUMBER: P66 38150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                    TELEFAX: (213) 489-4210 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_RNA
LOCATION: (5071)..(6085)
OTHER INFORMATION: ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: misc_RNA
LOCATION: (4013)..(4999)
OTHER_INFORMATION: ORF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 444 CONTROL OF CITY: LOS Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
TITLE OF INVENTION: Vector and Transformed Cell Thereof, and Expression Thereo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3243 ccgctggctcaccctcggccagatcgccgaactgctgcacgaggacgacctggtcaacat 3302
                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 622-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                         FEATURE:
                                                         TOPOLOGY: 1i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compation operating SYSTEM: PC-DOS SOFTWARE: Patentin Release SOFTWARE: Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 cccatttcccaagctgggctggggatgacggaactgcgggaaacccgggcgcccagatctacat 74
                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
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NAME/KEY:
                                                                                                                                          LENGTH:
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                                                                                                                                        2980 base pairs
                                                                               linear
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Pred. No. 17;
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US-08-462-390B-13/c
                RESULT
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US-08-461-379A-13
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Best Local S
Matches 33
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Best Local :
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INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,379A
FILING DATE: 5-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/330,108; 08/104,736
APPLICATION NUMBER: 6 07/796,066
APPLICATION NUMBER: 6 07/796,066
FILING DATE: 27-OCT-1994; 10-AUG-1993 & 20-NOV-91
                                                             2119
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Smith, Kendall A. & Beadling
TITLE OF INVENTION: Nucleic Acids Encoc
TITLE OF INVENTION: Vector and Transfor
TITLE OF INVENTION: Spression Thereof
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph.
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CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                          COMPUTER: IBM PC compatible OPERATING SYSEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, SOFTWARE: Version #1.25
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                                                                                                                                        Local Similarity
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Nucleic Acids Encoding CR5 Polypeptide,
Pector and Transformed Cell Thereof, and
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71.7%;
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71.7%;
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Pred. No. 22;
0; Mismatches
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Pred. No. 22;
                                                                                                                        Mismatches
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RESULT 9
US-08-463-074B-13/c
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PRIOR APPLICATION DATA: USSN 08/330,108
APPLICATION NUMBER: USSN 08/330,108
FILING DATE: 7-OCT-1994
APPLICATION NUMBER: USSN 08/104,736
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USSN 07/796,066
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                            NUMBER OF SEQUENCES: 3
                                                                                                                                     TITLE OF INVENTION:
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FEATURE:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)407-0700
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ATTORNEY/AGENT INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                CITY: Los Angeles
STATE: California
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STATE: Pennsylvania
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ADDRESSEE: . (B) STREET:One Westlakes-Berwyn
COUNTRY:
                                                         ADDRESSEE:
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                                                                              ADDRESSEE:
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USA
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                                                                                                                                                        Smith, Kendall A. & Beadling, Carol
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                                                       PRETTY, SCHROEDER & POPLAWSKI
(B) STREET:
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                                                                                                                                   Nucleic Acids Encoding
                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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Pred. No. 22;
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                                                                                                                                     CR1 Fusion Protein, Vector an
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                                                         444 South Flower St. - Suite 1
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APPLICATION NUMBER: US/08/465,585C
FILING DATE: 5-JUNE-1995
PRIOR APPLICATION NOTA:
APPLICATION NUMBER: USSN 08/330,108
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: USSN 08/104,736
FILING DATE: 10-AUG-1993
                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                          APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR6 Polypeptide, Vecto
TITLE OF INVENTION: Transformed Cell Thereof, and Expression There
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 20 NOV-91
ATTOKNEY/AGENT INFORMATION:
NAME: VIVIANA AMZE!, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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LENGTH: 2980 base pairs
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TELEPHONE: (213) 622-7700
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APPLICATION NUMBER:
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FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/104,736
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: Californiaa
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                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 900071
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Pred. No. 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (213) 4894210
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 2980 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Rel
SOFTWARE: Version #1.2
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: USSN 07/796,066
FILING DATE: 20.NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, ph. D.
REGISTRATION NUMBER: 30,930
                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,108
FILING DATE: 27-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
TITLE OF INVENTION:
                PRIOR APPLICATION DATA:
                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                              PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: cDNA
                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 ttcccaagctgggctgggatgacgaactgcggaaacccggcgccca
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nes 33; Conserv
                                             APPLICATION NUMBER:
                                                                                                                                                                            FILING DATE: 5-JUN-1996
                                                                                                                                                                                          APPLICATION NUMBER: PCT,
                                                                                                                                                                                                            APPLICATION NUMBER: 5-JAN
                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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Version #1.25
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                                                                             JMBER: 08/463,074
5-JUN-1995
                                5-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kendall A. & Beadling, Carol
I Nucleic Acids Encoding CR5
Polypeptide, Vector and Transformed Cell Thereof, and
Expression Thereof
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71.7%;
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08/462,390
                                           08/462,337
                                                                                                                                                                                                                      EP App. # 96921319.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (B) STREET:
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Pred. No. 22;
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Suite

FILING DATE:

5-JUN-1995

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; NAME/KEY: Modified base ; OTHER INFORMATION: n represents US-08-990-823-31
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; LOCATION:
US-08-652-446-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-990-823-31
Query Match
Best Local Similarity
Matches 53; Conserv
                                                                                                                                                                                            SOFTWARE: PatentIN Ver. 2.0 SEQ ID NO 31 LENGTH: 255
                                                                                                                                                                                                                                         APPLICANT: Nano, Francis

TITLE OF INVENTION: impurobacterium Tuberculosis DNA Sequences Encoding

TITLE OF INVENTION: immunostimulatory Peptides

FILE REFERENCE: 49086

CURRENT APPLICATION NUMBER: US/08/990,823D

CURRENT FILING DATE: 1997-12-15

EARLIER APPLICATION NUMBER: US 96/10375

EARLIER FILING DATE: 1996-06-14

EARLIER APPLICATION NUMBER: 60/000,254

EARLIER FILING DATE: 1995-06-15

NUMBER: 05 SEQ ID NOS: 113

COURTMENTS DESCRIPTION OF SEQ ID NOS: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 31, Application US/08990823D Patent No. 6228371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/739,523
FILING DATE: 29-0CT-1996
ATTORNEY/AGENT INFORMATION:
NAME: VIVIANA AMZEL, Ph. D.
RECISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: 7966 40035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (213) 489-4210
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                          ORGANISM: Mycobacterium tuberculosis FEATURE:
                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2119 TTCCGAGGCAGGGGTGGGGAGCCAGACCTGCGGAAACCCTCCCCCAA 2074
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FILING DATE: 5-JUN-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: CDNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 5-JUN-1 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 ttcccaagctgggctgggatgacgaactgcggaaacccggcgccca 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/463,081 FILING DATE: 5-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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   Conservative
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240..1475
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71.7%;
                    24.6%;
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                  Score 24.8;
Pred. No. 17
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Pred. No. 22;
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 Mismatches
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                                Length 255;
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Indels
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0;
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Gaps
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RESULT 14
PCT-US93-06251-65/c
Sequence 65, Application PC/TUS9306251
GENERAL INFORMATION:
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Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US
FILING DATE: September
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 83
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: MONACO, Daniel A.
REGISTRATION NUMBER: 30,480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: WordPerfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Calabretta, Bruno APPLICANT: Skorski, Tomasz TITLE OF INVENTION: ANTISENSE TITLE OF INVENTION: OLIGONUCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic
STRANDEDNESS:
TOPOLOGY: line
                                                                                                     469 CTGCTCCAGCTCCATGTGGCGGTAGAGCTGCT 438
                                                                                                                                                                   529 GGAGACCTGGTGGCCAAGACTGGGATGGGGTGCCACCATGGGGGGTATCGAGGACGTGCAT 470
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                                                                                                                        69 ctacatgcgcttcatgcaggagcacacctgct 100
                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PS,
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: Two Penn Control Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 cccagatctacatgcgcttcatgcaggagcacacctgcta 101
                                                                                                                                                                                             9 gcaggccccatttcccaagctgggctgggatgacgaactgcggaaacccggcgcccagat 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                   1364 base pairs
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Two Penn Center, Suite 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U.S.A.
                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                     linear
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N: 514
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OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
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ber 15, 1994
                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                  Score 24.8;
Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8321-8
                                                                                                                                                                                                                                                                  DB 1;
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                                                                                                                                                                                                                                                                  Length 1364;
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                                                                                                                                                                                                                                 Gaps
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APPLICANT:

Wickstrom, Eric and Rife,

Jason

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GENERAL INC.

APPLICANT: Mulero, Julio
APPLICANT: Mulero, Julio
APPLICANT: Weung, George
CAPPLICANT: Yeung, George
FITTLE OF INVENTION: METHODS AND MATERIALS RELATING TO CENTRE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 28110/36570
CURRENT APPLICATION NUMBER: US/09/608,285A
CURRENT FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/583,231
PRIOR APPLICATION NUMBER: 09/557,800
PRIOR APPLICATION NUMBER: 09/557,800
PRIOR APPLICATION NUMBER: 09/481,238
PRIOR APPLICATION NUMBER: 09/481,238
PRIOR APPLICATION NUMBER: 09/370,265
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: 09/370,265
PRIOR FILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: 0970-16
                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
US-09-608-285A-47/c
: Sequence 47, Application US/09608285A
: Patent No. 6335013
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: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
PCT-US93-06251-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06251
FILING DATE: 1933630
CLASSIFICATION:
ATTORNEY/AGFNYM -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity
Matches 50; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
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REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 85
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; TYPE: DNA
; ORGANISM: Homo sapiens
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Best Local Similarity
Matches 53; Conserv
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PRIOR APPLICATION NUMBER: 09/
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PRIOR APPLICATION NUMBER: 09/
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                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 09/
PRIOR FILING DATE: 1999-07-09/
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 491
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               61 gcccagatctacatgcgcttcatgcaggagcacacctgct 100
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AX099774
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AX099800
ALIGNMENTS
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AJ249977 Homo sapi

AX099774 Sequence

AF214520 Sus scrof

AX099800 Sequence

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AX099801 Sequence

AX281580 Sequence

AX281580 Homo sapi

AC00974 Homo sapi

AC095460 Rattus no

AC095460 Rattus no

AC095066 Rattus no

AC095086 Rattus no

AC095080 Homo sapi

AR139104 Sequence

AF087875 Homo sapi

BC015283 Mus muscu

AL036761 Human DNA

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AC096427 Rattus no

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REFERENCE
AUTHORS
TITLE
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DEFINITION
ACCESSION
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KEYWORDS
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Sequence 5 from Patent I
AX281582
AX281582.1 GI:16608833
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                              (sites)
                                                                                                     ΑB
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                                                                      Location/Qualifiers
1. .1647
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AUTHORS
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Patent: WO 0120003-A 3 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA)
Andersson, Leif (SE); Looft, Christian (DE); Kalm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A. Rogel-Gaillard,C., lannuccelli,N., Gellin,J., le Ro
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1 (bases 1 to 2109)
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Milarity 100.
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                                                                                                                                                                                     /protein_id-"CAC35799.1"
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/td_xref="GI:13538811"
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YRTIODLGIGTFRDLAVYLETAPLITAPVIFTVDRTYSALPYVNECGQVYGLYSRFDVI
HLAAQQTYNHLDMSVGEALRORFILCLEGVLSCQPHESLGEVIDRIAREQVHRLVLVDE
TQHLLCYVSLSDIQALYLSPAGIDALGA"
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/db_xrefu"taxon:9606"
472. .1389
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LOGCFRPLVSISPNDSLFEAVYTLIKNRIHRLPVLDPVSGNVLHILTHKRLLKELHIE
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VGLYSRFDVIHLAAQQTYNHLDMSVGEALRQRTLCLEGVLSCQPHESLGEVIDRIARE
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Vertebrata;

Euteleostomi;

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mRNA, complete cds.
AF214519
AF214519.1 GI:8215681
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Same, and uses thereof
Patent: WO 0120003-A 29 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA)
Anderson, Leif (SE); Looft, Christian (DE); Kalm,
Location/Qualifiers
1. .2115
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AX099802
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AVVLETAPILTALDIFVDRRVSALPVNNCCGOVVGLYSRFDVIHLAAQOTYNHLDMSV
GEALRORTLCLEGVLSCOPHESLGEVIDRIAREQVHRLVLVDETQHLLGVVSLSDILQ
ALVLSPAGIDALGA"

4 622 c 562 g 471 t
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/db_xref="GI:13538837"
/db_xref="GI:13538837"
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SSTDDVELATEFPATEAWECELEGLLEERPALCLSPQAPFPKLGWDDELRKPGAQIYM
RFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLWDSKKQSFYGMLTI
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/db_xref="taxon:9606"
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Pred. No. 1e-20;
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                                                                                                                15 bp mRNA linear PRI 03-JUN-2000 protein kinase gamma subunit (PRKAG3)
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Best Local
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                                  Homo sapiens
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Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                   AMP-activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and Andersson, L. A mutation in PRKAG3 associated with excess glycogen content in pig
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                                                                                                                                                           HSA249977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish University of Agricultural Sciences, BMC box 597, Uppsala 751 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 288 (5469), 1248-1251 (2000)
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/prodein_id="AMP-activated protein kinase gamma subunit"
/prodein_id="AAF73987.1"
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EPPGGGEGPRSRPTAESTGLEATFPKTTPLAQADPAGVGTPPTGWDCLPSDCTASAAG
SSTDDVELATEFPATEAWECELEGLLEERPALCLSPQAFFKLGWDDELRKPGAQIYM
RFMQEHTCYDAMATSSKLVIFOTMLEIKKAFFALVANGYRAAPLWDSKKQSFVGMLTI
TDFILVLHRYYRSPLVQIYEIEQHKIETWREIYLGGCFKPLVSISPNDSLFEAVYTLI
KNRIHRLPVLGPVSGNVLHILTHKRLLKFLHIRGSLLPRRSFILYATIQDLGIGTFRDL
AVVLETAPILTALDIFVDRRYSALPVNUECGGOVGLYSRFDVIHLAAQGTYNHLDMSV
GEALRGRTLCLEGVLSCQPHESJGEVIDRIAREGVHRLVLDETQHLLGVVSLSDILQ
ALVLSPAGIDALGA"
ALVLSPAGIDALGA"
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/db_xref="taxon:9606"
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Pred. No. 1e-20;
Mismatches
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Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Matches 101;
                                                                                                                              AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sus scrofa
Eukaryota;
Mammalia; E
Same, and uses thereof
Patent: WO 0120003-A 1 22-MAR-2001;
INSTITUT MATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA)
Andersson, Leif (SE); Looft, Christian (DE); Kalm,
                                                                                         1 (bases 1 to 1867)
Andersson, L. Looft, C., Kalm, E., Milan, D., Rot Rogel-Gaillard, C., Iannuccelli, N., Gellin, J., Chardon, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cheung, P.C., Salt, I.P., Davies, S.P., Hardie, D.G. and Carling, D. Characterization of AMP-activated protein kinase gamma-subunit isoforms and their role in AMP binding Biochem. J. 346 Pt 3, 659-669 (2000)
                                                                                                                                                                                                                   pig.
                                                                                                                                                                                                                                                                       Sequence 1 from AX099774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (12-OCT-1999) Carling D., Cellular Stress Group, MClinical Sciences Centre, Hammersmith Hospital, DuCane Road, London, W12 ONN, UNITED KINGDOM
                                                                      Variants of the gamma chain of ampk, dna
                                                                                                                                                                                                                                                      AX099774.1
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/product="AMP-activated protein kinase gamma 3 subunit"
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VGLYSRFDVHLAAAOCTYNHLDMSVGEALRKRTLCLEGVLSCOPHESLGEVIDRIARE
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22. .1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="AMPK gamma 3"
/function="AMP-activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                             Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Cetartiodactyla; Suina; Suidae;
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Patent WO0120003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 101; DB 9;
Pred. No. 1e-20;
; Mismatches 0;
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J., le Roy
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Sus.
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Best Local :
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                                                                                                                                                                        Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, University of Agricultural Sciences, BMC box 597, Uppsala
                                                                                                                                                                                                                      2 (bases 1 to 1873)
Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A.,
Rogel-Gaillard,C., Paul,S., Gellin,J., Lundstrom,K.,
Kalm,E., Le Roy,P., Chardon,P. and Andersson,L.
proof Computering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA, COM
AF214520
                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                     skeletal muscle
Science 288 (5469), 1248-1251 (2000)
                                                                                                                                                                                                                                                                                                                                                and Andersson,L.
A mutation in PRKAG3 associated with excess glycogen content in pig
                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 1873)
Milan,D., Jeon,J.T., Looft,C., Amarger,V., Robic,A., Thelander,M.,
Rogel-Gaillard,C., Paul,S., Iannuccelli,N., Rask,L., Ronne,H.,
Lundstrom,K., Reinsch,N., Gellin,J., Kalm,E., Roy,P.L., Chardon,P.
                                                                                                                                                               Sweden
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Cetartiodactyla: Suina: Suidae: Sus.
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Sus scrofa
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YRTIODLGIGTFRDLAVVLETAPILTALDIFVDRRVSALPVVMETGQVVGLYSRFDVI
HLAAQQTYNHLDMNVGFALRORTLCLEGVLSCOPHETLGEVIDRIVREQVHRLVLVDE
TQHLLGVVSLSOILQALVLSPAGIDALGA"

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472. .1389
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1. .1873
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                                                                                                                             Location/Qualifiers
1. .1873
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l. .1867
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96.0%;
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Sequence
AX099800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PATENT: WO 0120003 A 27 22-MAR-2001;
PATENT: WO 0120003 A 27 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR)
ANDERSSON, Leif (SE); Looft, Christian (DE); Kalm, Ernst
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Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             same, and uses thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Variants of the gamma chain of ampk, dna sequences encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Andersson,L., Looft,C., Kalm,E., Milan,D., Robic,A., Rogel-Gaillard,C., Iannuccelli,N., Gellin,J., le Roy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia;
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mmalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
(bases 1 to 1873)
  382
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ALVLSPAGIDALGA"
580 c 53
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TDFILVLHRYYRSPLYQIYEIEEHKIETWREIYLOGCFKPLVSISPNDSLFEAVYALI
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                                                                         KNRIHRLPVLDPVSGAVLHILTHKRLLKFLHIFGTLLPRPSFLYRTIQDLGIGTFRDL
AVVLETAPILTALDIFVDRRVSALPVVNETGQVVGLYSRFDVIHLAAQQTYNHLDMNV
                                             GEALRORTLCLEGVLSCOPHETLGEVIDRIVREQVHRLVLVDETQHLLGVVSLSDILG
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/translation="MSFLEQGESRSWPSRAVTTSSERSHGDQGNKASRWTRQEDVEEG
/translation="MSFLEQGESRSWPSRAVTTSSERSHGDQGNKASRWTRQEDVEEG
/translation="MSFLEQGESRSWPSRAVTLAQAAPLAEVDNPPTERDILPSDCAASAS
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                                                                                                                                                                                                                                                                                                                                             /note="unnamed protein product"
                                                                                                                                                                                                                                                                                                                                                                                                   organism="Sus scrofa"/db_xref="taxon:9823"
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Pred. No. 1.9e-18;
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Sequence 3 from Patent WO0177305
AX281580
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Sequence 31 from Patent
AX099804
                                                      Variants of the human amp-activated protein kinase gamma 3 Patent: WO 0177305-A 3 18-OCT-2001;
                                                                               Andersson, L., Luthman, H. and Marklund, S
                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                      Homo sapiens
                                                                                                                                                                             AX281580.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent: WO 0120003-A 31 22-MAR-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA)
Andersson, Leif (SE); Looft, Christian (DE); Kalm,
Location/Qualifiers
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    /organism="Homo sapiens"
                  Location/Qualifiers
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/db_xref="taxon:9823"
623 c 593 g
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Best Local :
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                                                                                                                                                                                                               Direct Submission
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Birren,B., Linton,L., Nusbaum,C
Homo sapiens, clone RP11-504G11
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Homo sapiens clone RP11-504G11,
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                      Center project name: L7458 Center clone name: 504_G_11
                                                                                         Center code: WIBR
                                                                             Web site: http://www-seq.wi.mit.edu
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504 c 534 g
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Summary Statistics vector: M13; M77815;
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Sanderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Anderson, S., Linton, L., Boukhgalter, B., Brown, A., Burkett, G., Collyson, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Keratas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Mencus, L., Mihova, T., Miranda, C., Menga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T. M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Voung, G., Zainoun, J., Zimmer, A., and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 7, 2000 this sequence version replaced gi:7342115.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                           Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                          Center: Whitehead Institute/ MIT Center
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Pred. No. 4.9e-14;
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38280 42366: contig of 4087 bp in 1
42367 42466: gap of 100 bp
42467 44365: contig of 3899 bp in 1
46366 46465: gap of 100 bp
46366 46465: gap of 100 bp
51286 51385: gap of 4820 bp in le
51286 51385: gap of 100 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 bp
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15044 15143; gap of 100 bp
15144 17123; contig of 1980 bp
17124 17223; gap of 100 bp
17124 17223; gap of 100 bp
1726; contig of 980 bp
1727 19466; gap of 1980 bp
19467 19566; gap of 19566;
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Consensus quality: 135376 bases at least Q40
Consensus quality: 143264 bases at least Q30
Consensus quality: 146503 bases at least Q20
                                                                                                                73319 77115: contig of 3797 b
777116 77215: gap of 7797 b
777116 77215: gap of
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1006 1105: gap of 100 bp
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3924 5020: con
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7547: r
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                                   93414:
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38179: contig of 4111 bp
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7647: gap of 100 bp
9983: contig of 2336 bp
10083: gap of 100 bp
12556: contig of 2473 bp
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3823: cor
          414: gap of
101193: con
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93314: contig of 8192 bp in
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85022: contig of 7807 b
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55871: contig of 4486 k
371: gap of 100 bp
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137938 152129: contig of 14192 bp
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85123. .93314
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5121, .6161
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101294. .113090
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93415. .101193
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Sequencing vector: plasmid; 0%
Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 98% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: phrap; version 0.990319
Consensus quality: 187795 bases at least Q40
Consensus quality: 190513 bases at least Q30
Consensus quality: 192099 bases at least Q20
Insert size: 200000; agarose-fp
Insert size: 194954; sum-of-contigs
Quality coverage: 5.58 in Q20 bases; sum-of-contigs
Quality coverage: 5.567 in Q20 bases; sum-of-contigs
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On Feb 21, 2001 this sequence version replaced gi:8469048.
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Waterston, R.H.
Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
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                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence of Homo sapiens clone
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AC073128
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   1157: contig of 1157 t
1257: gap of unknown 1
3600: contig of 2343 t
3700: gap of unknown 1
5103: contig of 1403 t
5203: gap of unknown 1
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91.3%; Pred. No. 5.1e-14;
tive 0; Mismatches 8
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                                         clone_end:SP6
                                                                         /note="assembly_name:Contig32
149388. .196554
                                                                                                                                    /note="assembly_name:Contig30"
113438. .130325
                                                                                                                                                                      73917. .92140
/note="assembly_name:Contig29"
92241. .113337
                                                                                                                                                                                                                                                               35356. .44642
/note="assembly_name:Contig26"
44743. .58275
                                                                                                                                                                                                                                 /note="assembly_name:Contig27"
58376. .73816
                                                                                                                                                                                                                                                                                                                                                                                          /note="assembly_name:Contig22" 15884. .21906
                                                     /note="assembly_name:Contig33
                                                                                                      /note="assembly_name:Contig31"
130426. .149287
                                                                                                                                                                                                               /note-"assembly_name:Contig28"
                                                                                                                                                                                                                                                                                                                             /note="assembly_name:Contig24"
28988. .35255
                                                                                                                                                                                                                                                                                                                                                                                                                           /note="assembly_name:Contig21"
11957. .15783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vector_side:right"
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/db_xref="taxon:9606"
/chromosome="2"
                                                                                                                                                                                                                                                                                                          /note="assembly_name:Contig25"
                                                                                                                                                                                                                                                                                                                                                            /note="assembly_name:Contig23"
22007. .28887
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/note="assembly_name:Contig18"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="assembly_name:Contig19
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contig of 21097 bp in 1
gap of unknown length
contig of 16888 bp in 1
contig of 16888 bp in 1
contig of 18862 bp in 1
gap of unknown length
contig of 47167 bp in 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gap of unknown contig of 6023 and of unknown contig of 6881
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contig of 15441 bp in
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                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (03-JAN-2002) Genome
University School of Medicine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MO 63108,
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Homo sapiens BAC clone RP11-459119
AC009974
AC009974.9 GI:16799050
                                                                                                                                                                                                                   Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 6 On Nov 8, 2001 this sequence version replaced gi:13431203.
                                                                                                                                                                                                                                                                                                       MO 63108, USA
6 (bases 1 to 206854)
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5 (bases 1 to 206854)
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                                                                                                                                                                                                                                                                                            Waterston, R.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                   Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                                                     Center project name:
                                                                                                                                                                     Center: Washington University Genome Sequencing Center Center code: WUGSC
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91.38;
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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >- 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. I MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc Sinor

donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E., Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:18. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu)
VECTOR: pBAC63.6

NEIGHBORING SEQUENCE INFORMATION: The clone sequenced to the left is RP11-1077K22; the clone sequenced to the right is RP11-64705. Actual start of this clone is at base position 1 of RP11-459119; actual end is at base position 206854 of RP11-459119.

Data from AC079810 and AC073128 was used to finish this clone, AC009974. Polymorphisms have been identified between AC073128 AC009974. A single plasmid region exists betten 38812-38903 unresolved tandem in the HERV SVA exists between 184390-185163. PCR suggests that approximately 1700 bps are missing. ₹ and

FEATURES

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/chromosome="2" /note-1. .206854 /note="match /note="match /note="match /note="match /note-"match /note-"match /clone="RP11-459I19" /clone_lib="RPCI-11" /map="2" note="match /note="match to /note="match to EST BE314060 (NID:g9134719)" "match to match ç ţ ç ö ç ő to ö EST BI059713 (NID:g14467240)" Homo BF304755 (NID:g11251653)" C05773 (NID:g1502549)" AI670836 BE047599 (NID: 98364652) tz39c01.y1* BG477625 (NID:g13409904)* AW880850 (NID: 98042860) " AL567345 (NID:g12920610)" BF183086 (NID:g11061273)* sapiens (NID:g4850567) wa04g10.x1" (NID:g10402954)" EST BI114348

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (10-DEC-1999) Dept Animal Breeding and Genetics, Swedish University of Agricultural Sciences, BMC Box 597, Uppsala 751 24,
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HFMQEHTCYDAMATSSKLVIFDTMLEIKKAFFALVANGVRAAPLADSKKQSFVGHLTI
TDFILVLHRYYRSPLVQIYEIEEHKIETWREIYLQGCFKPLVSISPNDSLFEAVYALI
                      ALVLSPAGIDALGA"
                                       AVVLETAPILTALDIFVDRRVSALPVVNETGQVVGLYSRFDVIHLAAQQTYNHLDMNV
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/db_xref="GI:8215686"
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                                                                                                                                                   Matches
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5471 ACATTCCGAGATTTGGCTG 5453
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                     acattccgagacttggctg 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (17-JAN-2001) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus l (bases 1 to 227724) Rump,A., Hayes,C., Brown,S.D.M. and Rosenthal,A. Mouse chromosome 1 genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rump, A.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF336381 227724 bp DNA linear HTG 02-APR-2001 Mus musculus chromosome 1 clone PAC510; PAC457, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.
                                                                                                                                               Similarity 93.7
74; Conservative
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32847
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/clone="PAC510; PAC457"
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55423 c 56238 g 58199 t
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/organism="Mus musculus"
/db_xref="taxon:10090"
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                                                                                                                                          70.3%; Score 71; DB 2; Length 227724; 93.7%; Pred. No. 1.7e-11; tive 0; Mismatches 5; Indels 0
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Search completed: October 3, 2002, 14:50:23 Job time: 12143 sec

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2: //SIDS1/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
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Copyright (c) 1993 - 2000 Comp
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                                                       score distribution
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AAS95361	99	96	AAV18471	538		826	ABL21170	ABL06404	AAS77333	AAH15945	7	AAC39424	ABL06405	AAL02279	AAC98901	AAK81195	AAK76548	AAK81194	AAF64424	ABL04284	ABL02824	ABL02825	ABL07646	ABL07647	AAS17159	AAV63702	AAV19135	AAQ51226	AAS17161	ABL08198	19	23	55	483	AAS84265
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ALIGNMENTS

RESULT ABA08485 Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopolesis regulation; tissue growth; immunomodulator; activin; inhibin, chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoletic disorder; myeloid cell disorder; jymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; antifungal; 05-FEB-2001; 2001WO-US03800 WO200157188-A2 Homo sapiens. Human AMP-activated protein kinase subunit homologue cDNA, 11-JAN-2002 (first entry) ABA08485 standard; cDNA; 547 ABA08485; vulnerary; osteopathic; vasotropic; cardiant; virucide; antibacterial; ВP

SEQ ID NO:261.

Result

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Score

Match Query

Length

DB

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Description

ABA08485

01010

93.6 93.6 93.6 79.2

100.0 100.0 100.0 100.0 92.7 92.7 92.7 92.7 92.7 92.7

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Human AMPK gamma s Human AMPK gamma s Human AMP-activate PRKAG3 cDNA. Homo

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                                                                                                                                                                                                                                                                                                     Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and CC sequences ABA0825-ABA09574 represent nucleic acids encoding them. The CC invention also relates to vectors and recombinant host cells comprising a CC antibodies against the polypeptides, methods of producing the novel polypeptides, cor polypeptides in a sample, and methods of identifying compounds which CC polypeptides of the invention have homology to known proteins, thereby cor giving an insight into their probable biological activities, and hence CC potential therapeutic applications. The polypeptides of the invention have homology to known proteins, thereby cor differentiation activities; stem cell growth factor activity. CC immunomodulatory activity; activing these growth activities; and hence cc have various activities; stem cell growth factor activity. CC immunomodulatory activity; activing these growth activities; or may be immunomodulatory activity; activity tissue growth activities; or may be consisted in oncogenesis. Cancer cell proliferation or metastasis. CC thrombotytic activity, activities; had hence cc involved in oncogenesis. Cancer cell proliferation or metastasis. CC disorders, heamatopoletic disorders (e.g., myeloid or lymphoid cell conditions, e.g., by protein or gene therapy. Such conditions include cancers, heamatopoletic disorders (e.g., myeloid or lymphoid cell. CC disorders, chronic inflammatory conditions (e.g., asthma or arthritis), cromary heart disease, arterial ischaemia, bone disorders (e.g., myeloid or lymphoid cell. CC disorders, chronic inflammatory conditions (e.g., asthma or arthritis), cromary heart disease, arterial ischaemia, bone disorders (e.g., myeloid or lymphoid cell. CC disorders, include sincer cell growth. Folypeptides included in the tissue regeneration and crepair (or nucleic acids encoding them) may be used to promote wound included to myelong them in the tissue regeneration and cell cancers with growth factor activity may be used in cell cultures to cell growth. For or example, such po
RESULT
                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                   03-FEB-2000;
27-APR-2000;
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                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                         547 BP; 112 A; 172 C; 133 G; 130 T; 0 other;
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2000US-0560875.
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AAH43685

AAH43685 standard;

CDNA; 1647 BP

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Matches

101;

0

Mismatches

0;

Indels

0

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Query Match
Best Local
                                                                                             This sequence represents the full length cDNA encoding the human AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution P71A; in exon 4 variation may be a substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution R340W. There may also be nucleotide variation in intron 6. The numbering of these variations is based on the full length cDNA as given, rather than on
                                                              Sequence 1647 BP; 346 A; 502 C; 462 G;
                                                                                                                                                                                                                                                                                                                 New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and metabor determining a risk estimate of diseases in subject by detecting
                                                                                                                                                                                                                                                                             Disclosure; Fig 5; 25pp; English.
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/note= "Causes R340W"
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(AMP) activated kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3. Mutation in PrKag3 results in an altered regulation of pRKAG3. Mutation in PrKag3 results in an altered regulation of suseful as therapeutic for treating carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as disposably, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic evaluation, genetic testing and prognosis of a metabolic disorder, primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are
                                                                                                   The present sequence is a cDNA encoding human adenosine monophosphate
                                                                                                                         Claim 12; Fig
                                                                                                                                               New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of associated with energy metabolism such as diabetes, obesity,
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Query Match
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New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
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18-MAY-2000;
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Iannuccelli N,
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cystathione beta synthase; CBS; cardiant; gene therapy; RN locus;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is a cDNA encoding pig adenosine monophosphate (C PRKAG3. PrKag3 gene is located in the RN locus of chromosome 15. CC Mutation in Prkag3 gene is located in the RN locus of chromosome 15. CC Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as CC diabetes, obesity, and disorders associated with muscle metabolism CC such as myopathy and cardiovascular diseases, to modulate AMPK CC activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic CC evaluation, genetic testing and prognosis of a metabolic disorder. CC preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting CC from the expression of a functionally altered allele of PRKAG3. CC Transgenic animal and host cell transformed with PRKAG3 or a heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for cscreening compounds able to modulate AMPK activity. Nucleic acid consisting of PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain confidence in a sequence encoding the first cystathione beta synthase (CBS) domain the first cystathione beta synthase (CBS) domain confidence there are a sequence and the presence of the presence of the presence of the presence and the presence of the presence and the presence of the presence and t
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         Pig AMPK gamma subunit muscle-specific isoform,
                                                                                                                                                             13-JUN-2001
                                                                                                                                                                                               AAD03319;
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(ANDE/) ANDERSSON L
(LOOF/) LOOFT C.
(KALM/) KALM E.
                                                                                                                                                                                                                               AAD03319 standard; cDNA; 1873 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1867 BP; 380 A; 583 C; 529 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New variants of the gamma subunit of vertebrate adenosine monophosphate activated kinase for diagnosis or treatment associated with energy metabolism such as diabetes, obesit
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Iannuccelli N,
                                                                                                                                                                                                                                                                                                                                62 atccaagatttgggcatcggcacattccgagacttggctg
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                                                                                                                                                         (first entry)
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V, Gellin
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96.08;
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J, Le
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→ Roy
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Pred. No. 2
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≀oy P, C
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Chardon P;
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Best Local
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Transgenic animal and host cell transformed with PRKAG3 or a heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                  such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence activity, and for restoring a normal ampK functionally altered mutants are useful for the diagnostic
                                                                                                                                                                                                                                                                                                                                                                                        (AMP) activated kinase (AMPK) gamma subunit muscle-specific isoform, complete PRKAG3. Prkag3 gene is located in the RN locus of chromosome 15. Mutation in Prkag3 results in altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism
                                                                                                                                                                                Sequence 1873
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        967
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Iannuccelli N,
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18-MAY-2000;
scrofa
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1..1395
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                                                                                                                         92.78;
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                                                                                                                                                                             580 C;
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                                                                                                                         Score 93.6;
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don P;
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                                                                                                                                   Length
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                                                                                                                                    1873;
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AAD03321
ID AAD
                          evaluation, genetic testing and prognosis of a metabolic disorder, preferably a carbohydrate metabolism disorder. Primers that can detect a genetic polymorphic marker linked to a sequence encoding PRKAG3, are useful for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of PRKAG3. Transgenic animal and host cell transformed with PRKAG3 or a heterotrimeric AMPK consisting of PRKAG3 or its mutant, are useful for screening compounds able to modulate AMPK activity. Nucleic acid encoding PRKAG3 is useful for detecting mutations in a Prkag3 gene, or in a sequence encoding the first cystathione beta synthase (CBS) domain of PRKAG3 and is useful in gene therapy.
                                                                                                                                                                                                       The present sequence is pig adenosine monophosphate (AMP)-activated kinase (AMPK) gamma subunit muscle-specific isoform, PRKAG3 splice variant DNA. Prkag3 gene is located in the RN locus of chromosome 15 Mutation in Prkag3 results in an altered regulation of carbohydrate metabolism, particularly in skeletal muscle. PRKAG3 is useful as therapeutic for treating carbohydrate metabolism disorders such as diabetes, obesity, and disorders associated with muscle metabolism such as myopathy and cardiovascular diseases, to modulate AMPK activity, and for restoring a normal AMPK function. PRKAG3 sequence and its functionally altered mutants are useful for the diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                       New variants of the gamma subunit of vertebrate adenosine monophosphate-activated kinase for diagnosis or treatment of disorders associated with energy metabolism such as diabetes, obesity, and
                                                                                                                                                                                                                                                                                                                                                                                              Claim 12; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                 myopathy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (INRG ) INRA INST NAT RECH AGRONOMIQUE (ANDE/) ANDERSSON L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-SEP-1999;
18-MAY-2000;
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DB; AAE00224.
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LOOFT C.
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Gellin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rogel-Gaillard C;
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Sequence 2022

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412 A;

623 C;

593 G;

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                                                                                                                                              intron
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                                                                                                 /number= "Intron 987. 1041
                                                         /"tag= )
/number= "Exon
1370..1522
                   /number= "Intron 10"
                                  /number= "Exon
                                           /"Lay" k
/number= "Intron
1523..1688
                                                                                                                 /number= "Exon
783..986
                                                                                                                                /number= "Intron 6"
737..782
                                                                                                                                                            553..611
                                                                                                                                                                          /number= "Exon 96..552
                             689..1722
                                       /*tag=
                                                                        1243..1369
                                                                            /number= "Intron
                                                                                /*tag=
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                                                                                                                                                                                        /note= "3' portion of intron 14..95
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96.08;
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Pred. No. 2.4e-20;
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RESULT
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Best Local S
Matches 84
   Homo sapiens
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DAPK-7; disease associated protein kinase; human; diagnosis; therapy; adult respiratory distress syndrome; allergy; asthma; arteriosclerosis; bronchitis; emphysema; hypereosinophilia; myocardial inflammation; pericardial inflammation; anaemia; rheumatoid arthritis; Addison's disease; AIDS; atherosclerosis; atopic dermatitis; dermatomyositis; diabetes mellitus; glomerulonephritis; gout; Grave's disease; lupus erythematosus; multiple sclerosis; myasthenia gravis; osteoarthritis; osteoporosis; pancreatitis; polycystic kidney disease; polymyositis; scleroderma; Sjorgren's syndrome;
                     autoimmune thyroiditis; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequences given in AAH43681-84 represents genomic fragments encoding the human AMP-activated protein kinase gamma 3 subunit (PRKAG3). Detecting the presence of the PRKAG3 DNA, or a variant, is useful in determining a risk estimate of a metabolic disease, such as diabetes or obesity, in a subject. The variation may occur in exons 3, 4 or 10. In exon 3 variation may be a substitution of a G for a C at nucleotide 320, resulting in the amino acid substitution P71A; in exon 4 variation may be a substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a T for a C at nucleotide 550; and in exon 10 variation may be a substitution of a T for a C at nucleotide 1037, resulting in the amino acid substitution R340W. There may also be nucleotide variation in intron 6.
                                                                                                                                                                                                                                                                                                                                                                                             26-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX06882 standard; cDNA; 1435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1570 tttgggcatcggcacattccgagacttggctg 1601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New variants of human AMP-activated protein kinase gamma3 subunit associated with a metabolic disease e.g. diabetes or obesity and metabolic diseases in subject by detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AREX-) AREXIS
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proliferation;
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                                                                                                                                                                                                                                                                                                                                      associated protein
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91.3%;
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                                                                                                                                                                                                                                                                                                                                      kinase DAPK-7 cDNA
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tecting the
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                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of the digestive system, atopic dermatitis, dermatomyositis, diabete mellitus, glomerulonephritis, gout, Grave's disease, lupus erythematosus, multiple sclerosis, myasthenia gravis, osteoarthritis, osteoporosis, panoreatitis, polycystic kidney disease, polymyositis, scleroderma, Sjorgren's syndrome, autoimmune thyrolditis, complications of cancer, extracorporal circulation, viral, bacterial, fungal, parasitic, protozoal and helminthic infections, and trauma (disclosed). The DAPK nucleic acids are also used in a method for detection of DAPK expression levels in a
                                                                                                                                                                                                            617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1435 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        biological sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the PENITUT01 cDNA library using a computer search for amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 5; Page 66-67; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New disease associated protein kinases - used to stimulate proliferation and to treat the immune response and cancer % \left( 1\right) =\left\{ 1\right\} =\left\{ 1\right
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
677 ctggatgagcttggaataggaacgtaccacaacattgc 714
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                                                               62 atccaagatttgggcatcggcacattccgagacttggc 99
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57.1%;
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Pred. No. 2.3;
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775 ctggatgagcttggaataggaacgtaccacaacattgc

62 atccaagatttgggcatcggcacattccgagacttggc

Conservative

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42;

Indels

0

Gaps

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CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC (II): (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess blodiversity
CC and to produce other types of data and products dependent on DNA and
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at fip. wipo.int/pub/published_pct_sequences.
                   Query Match
Best Local 9
                                                                                       Sequence 1467 BP; 416 A; 327 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID No 20069; 103pp; English
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23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder;
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                     Similarity
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2000US-0649167.
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57.1%;
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Score 30.8; DI
Pred. No. 2.3;
0; Mismatches
                                                                                       343 G;
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RESULT 11
AAH14839
AAH14839
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Matches 56
                                                                                                                                                                                                                               sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the the full-length cDNAs. The primers are also useful for the continuation of the full-length cDNAs. The primers are also useful for the the full-length cDNAs. The primers are also useful for the continuation of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH1872 represent human cDNA sequences; AAB02446 to AAB05893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the property invariance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5' end
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02-MAY-2000;
09-JUN-2000;
                                                                                                                                                          Sequence 2223 BP; 633 A; 431 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-318749/34.
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27-AUG-1999;
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                                            Similarity
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            Conservative
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2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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T, Wakamatsu
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                                     Score 30.8; DB Pred. No. 2.5;
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         Mismatches
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A, Nagai K,
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Best Local
                                                                                                                                                           vestibular system modulating activity. The DNA sequences can be used in method whereby a first and second strain of an invertebrate is obtained, and both are subjected to conditions in which the strains exhibit different geotactic behaviour. Genes that are differentially expressed in the first strain relative to the second strain are then identified. Mammalian genes having substantially the same nucleic acid sequence as these modulate the mammalian vestibular system. Compounds containing these genes are used to decrease the symptoms of graviperceptive disorders such as motion sickness, vertigo, labyrinthitis, Meniere's disease, acoustic neuroma, multiple sclerosis, syphilis, trauma, infection of the middle ear, exposure to ototoxic agents and epilepsy.
                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                    The sequences shown in AAS05401-AAS05661 represent DNA with mammalian
                                                                                                                                                                                                                                                                                                                                                                               Claim 59;
                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid having mammalian vestibular system-modulating activity useful in the treatment of disorders such as motion sickness
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalian vestibular system; invertebrate; geotactic behaviour; vertigo; graviperceptive disorder; motion sickness; labyrinthitis; syphilis; ds; Meniere's disease; acoustic neuroma; multiple sclerosis; epilepsy; trauma; infection of the middle ear; ototoxic agent exposure.
        544
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26-SEP-2000; 2000US-0669751.
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                                                                Local Similarity 68.
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GCTCATCAAAGGTGACTACCTGTTCCTGCTCTTCTTCCTCTACCTCATTATCCCTGATCT 485
              9Cacalctttggttccctgctgccccggccctccttcctctaccgcactatccaagattt 72
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31-AUG-1999
32-SEP-1999
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25-CCT-1999
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99US-015377
99US-0154039
99US-0155286
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99US-0150566.
                                                                                                          29.38;
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     WO200171042-A2
                                                                26-MAR-2002
                                                                            ABL08198;
                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                             Claim 1;
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                                                                                                                                                                                                                                                                                                                                      Venter JC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                        pharmaceutical;
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ABL08198/c
ID ABL08198 standard;
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                                 Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical; gene; ss.
Drosophila melanogaster.
                                                                                              Drosophila melanogaster expressed polynucleotide SEQ ID NO 19076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              specification, but was obtained in electroni
at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid genes from Drosophila and interactions -
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11-JUL-2000; 2000US-0614150
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nilarity 68.3%;
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Best Local Similarity 68.3%;
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                                                             The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                               Sequence 4363 BP; 1461 A; 939 C; 974 G; 989 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions - \,
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P-PSDB; ABB64095.
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B1774231	AA045087	AL581895	BH447226	BM340317	AI062937	AI062936	AQ535079	BI659310	AI063338	BF488250	BF528264	BE978092	AV525978	BG035134	AU080009	BG415737	CNS029MX	C06172	AL524822	AL513784	AL558594	BG572824	B1657718	AU138307	BE846246	BG148719	BI760420
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ALIGNMENTS

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REFERENCE
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                                                                                                                                         source
                                                                                                                                                                                                                                                                                  Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Fax: 402 762 4390
Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore and minmatch 12 options.
                                                                                                                                                                         BACKWARD: GTTTTCCCAGTCACGACG
Plate: 119 row: I column: 11
Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 572) Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Lægreid,W.W. and Keele,J.W.
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373008 MARC 2PIG Sus sc.
BI344527
BI344527.1 GI:15037807
                                                                                                                                                                                                                                PCR PRIMERS
FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST discovery in swine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Design and use of two pooled tissue normalized cDNA libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sus scrofa
                      /organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 2PIG"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       572 bp mRNA linear 2PIG Sus scrofa cDNA 5', mRNA sequence
pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin, J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     413 bp mRNA linear EST 09-MAR zp38d10.rl Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:611731 5' similar to SW:AAKG_RAT P80385 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA CHAIN ;, mRNA sequence
                                                                                                                                                                                                                                                                                                                                     Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                       white,Y., Wylie,T., Watersto
WashU-NCI human EST Project
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                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1997)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota: Metazoa: Chordata: Craniata; Vertebrata;
Mammalia; Eutheria: Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA178898
AA178898.1
            Similarity
                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 413)
                                                                                                                                                                                                                                                     quality sequence stop:
Location/Qualifiers
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                                                                 Library made endometrium, a 190 c
                                                                                                                                                            /clone-"IMAGE:611731"
/clone_11b-"Stratagene muscle 937209"
/tissue_type="muscle"
/dev_stage-"adult"
                                                                                                                                                                                                          /db_xref="taxon:9606"
                                                                                                                                                                                                                     /organism-"Homo sapiens"
/db_xref-"GDB:4643570"
 58.4%; Score 59;
100.0%; Pred. No.
tive 0; Mismatc
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   Mismatches
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131 CTCAAGTTCCTTCACCTCTTTGGTGACACTCTGCCTAGGCCACAGTTCTTGCAGAAGACC 190
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                                                                                                                                                                                                                                                                                                                                                                                                             AT CCTGGAGCTGGGCATCGGCACTTTCAGGGATATAGCAG
                                                                                                                                                                            BG037921
dc69g08.y1 i
5' similar i
BG037921
                                   Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; i
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
Xenopodinae; Xenopus.
1 (bases 1 to 514)
                                                                                                                      BG037921.1 GI:124805
EST.
African clawed frog.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center For Genetic Resource Information National Institute of Genetics IIII Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BJ072114 NIBB Mochii normalized Xenopus tailbud laevis cDNA clone XL096jl6 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2001)
Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Expressed genes in X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kitayama,A., Terasaka,C., Mochii,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopodinae; Xenopus.
1 (bases 1 to 633)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:8355"
/clone="xL096j16"
/clone= 11b "...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="whole embryo"
/dev_stage="stage 25"
162 c 148 g 179 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="NIBB Mochii normalized
                                                                                                                                                                                    NICHD XGC Embl Xenopus laevis CDNA clone IMAGE:3402446 to TR:Q9ULX8 Q9ULX8 H91620P. ;, mRNA sequence.
                                                                                                                                                              GI:12480506
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Pred. No. 0.0015;
0; Mismatches 3
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                                                                      Euteleostomi; 
; Pipidae;
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Pipidae;
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                                                                                             http://image.llnl.gov
Plate: LLAM10079 row: d column:
High quality sequence stop: 691.
                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

] (bases 1 to 918)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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BG027175
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Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LLNL at: Info@image.llnl.gov

Seq primer: -40Rp from Gibco

High quality sequence stop: 437.

Location/Qualifiers
                                                                                                                                                    found through the I.M.A.G.E. Consortium/LLNL
                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                               cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BG027175.1
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/db_xref="taxon:8355"
/clone="InAGE:3402446"
/clone=lib-"NICHD XGC Embl"
/fissue_type="embryo (stage 10)"
/lab_host="OH10B (phage resistant)"
/note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI;
Cloned unidirectionally. Primer: Oligo dT. Average insert
size 1.55 kb. Constructed by Life Technologies. Note: This
is a Xenopus Gene Collection (XGC) library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q,
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4390238"
                                                                         Location/Qualifiers
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AW147353/c
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Library normalized by Jihwan Song
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clone distribution information for
this library can be found through Research Genetics, visit their
web page at: http://www.resgen.com/
Seq primer: -40RP from Gibco
High quality sequence stop: 409.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ....., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D., Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Sandy Clifton, Ph.D.
WashU Xenopus EST project, 1999
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Other_ESTs: da01h11.x1 Contact: Sandy Clifton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WashU Xenopus EST project, 1999
Unpublished (1999)
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451 bp mkNA
da01h11.y1 Xenopus laevis oocyte Xenopus
XENOPUS_SOURCE_ID:xlnoc001d22 5' similar
                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; (
Amphibia; Batrachia;
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57; Conserv
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/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; cDNA was prepared from 2ug of poly A+ RNA. EcoRI-XhoI cut cDNA was then ligated into Unizap-XR
                                                                /clone="XENOPUS_SOURCE_ID:xlnoc001d22"
/clone_lib="Xenopus laevis occyte"
/tissue_type="occyte (stages 5 and 6)"
/lab_host="Top-10 F'"
                                                                                                                                                                      /organism="Xenopus laevis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="osteosarcoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="organ: bone: Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.533 kb. Library enriched for
full-length clones and constructed by Life Technologics.
Note: this is a NH_MGC Library."
a 138 c 263 g 258 t
                                                                                                                                                       /db_xref-"taxon:8355"
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Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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Matches 52
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                                                 l Similarity
52; Conserv
                                                                                                                                                                                                                                                                                                                                                       Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kitayama, A., Terasaka, C., Mochii, M.,
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Xenopus laevis
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BJ036397 NIBB Mochii normalized Xenopus neurula library Xenopus laevis CDNA clone XL036d24 5', mRNA sequence.
BJ036397
BJ036397
GT07736982
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Expressed genes in X. laevis embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopodinae; Xenopus.
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                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Stratagene) with EcoRI at the 5' end and xhoI at the 3' end. SS-library phagemids were prepared by mass excision from the original library and normalized by hybridization to biotinylated driver (prepared from the same library by PCR) to Cot-omega of 11. After removal of hybrids and excess driver by streptavidin sepharose chromatography, the ss-phagemids were made double stranded and electroporated into Top-10 F'. Original library contruction by Bruce Blumberg (Blumberg et al., 1991 Science 253, 194-196; Hawlet et al., 1995, Genes Dev. 9, 2923-2935). Normalized by Jihwan Song (Song, Cho and Blumberg, unpublished). Note: This is a Xenopus Gene Occlection (XGC) library."
                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                             D)
                                                                                                                                                 /tissue_type="whole embryo"
/dev_stage="stage 15"
108 c 112 g 101 t
                                                                                                                                                                                                                  library"
                                                                                                                                                                                                                       /clone_lib="NIBB Mochii normalized Xenopus neurula
                                                                                                                                                                                                                                                   /clone="XL036d24"
                                                                                                                                                                                                                                                                   /organism="Xenopus laevis"
/db_xref="taxon:8355"
                                                            31.9%;
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Pred. No. 47;
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Pred. No. 47;
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BG101440
BG101440.1
                                  house mouse.
Mus musculus
                                                                                                                           BG101440 684 bp mRNA linear EST 29-JAN-2001 uy72c12.yl McCarrey Eddy round spermatid Mus musculus cDNA clone IMAGE:3664919 5' similar to TR:09ULX8 Q9ULX8 H91620P. ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                   l Similarity 61.: 52; Conservative
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                       EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sato,K., Saisho,D. and Takeda,K.
Barley EST sequencing project in NIG and Okayama Univ
Unpublished (2002)
Contact: Tadasu Shin-i
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Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldea
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AV914030.1 GI:18209807
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Location/Qualifiers
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/clone_lib="K. Sato unpublished
Nijo germination shoots"
/tissue_type="shoots"
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137 c 141 g 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Hordeum vulgare /cultivar="Haruna Nijo" /db_xref="taxon:112509"
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Pred. No. 50;
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BM2008.921 Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate cDNA library (pgm2n) Gallus gallus cDNA clone pgm2n.pk008.921 5' similar to gblAAC52580.1 (U42413) 5'-AMP-activated protein kinase, gamma-1 subunit [Rattus norvegicus]
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This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Marra M/WashU-NCI Mouse EST Project 1999
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                             mRNA sequence.
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314 286 1810
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//lab_host="DilOB (strest) (phage-resistant)"
//lab_host="DilOB (strest) (phage-resistant) (pha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             quality sequence stop: 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genetics); excision done by E.M. Eddy, Ph.D. (National Institutes of Health, National Institute of Environmental Health Sciences). Original lambda-based library is available through ATCC, catalog #63423."

a 163 c 134 g 177 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="round spermatids, pooled from multiple mice"
/dev_stage="60 day"
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/strain="CD-1"
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                          GI:18609593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 atccaagatttgggcatcggcacattccgagacttggctg 101
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                                                                                                                                           Gallus gallus
                                                                                                                                                                                                                                                                                                     BM487789 S95 bp mRNA linear EST 07-FEB-: pgm2n.pk005.j24 Normalized Chicken Breast Muscle, Leg Muscle, ar Epiphyseal Growth Plate cDNA library (pgm2n) Gallus gallus cDNA clone pgm2n.pk005.j24 5' similar to gb|AAC52580.1 (U42413) 5'-AMP-activated protein kinase, gamma-1 subunit [Rattus norvegi
                                                     Archosauria; Aves; Neognathae; Phasianinae; Gallus.
                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
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chicken.
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Cogburn,L.A. and Monsonego-Ornan,E.
ESTs from Normalized Chicken Breast Muscle, Leg Muscle, and
Epiphyseal Growth Plate cDNA library, USDA/IFAFS Animal Genome
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Contact: Larry A.
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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                                                                                                                                                                                                                                                                                   mRNA sequence.
                                (bases 1 to 595)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pCMVSPORT6; Library made from equivalent pools of total RNA isolated from each tissue (embryonic muscle 33.3%; juvenile muscle 33.3%; and epiphyseal growth plate 33.3% of the final RNA pool). Single pass sequencing from 5'-end"

171 c 132 g 116 t
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/strain="Commercial broiler
Strains 90 & 21"
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,11 weeks);growth plate(1d,7d,14d post-hatch)"
/lab_host="E. coli EMDH10B"
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/clone_lib="Normalized Chicken Breast Muscle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="Breast muscle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref~"taxon:9031"
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location/Qualifiers
                                                                                                                                                                                                                              GI:18608720
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Monsonego-Ornan, E
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Pred. No. 92;
0; Mismatches
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(pgm2n)

Leg Muscle,

EST 07-FEB-2002

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Gaps

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AUTHORS
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Best Local
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Cogburn, L.A. and Nys, Y.
EST's from Normalized Chicken Reproductive Tract cDNA library-
University of Delaware and INRA, Tours-Poultry Unit Project
Unpublished (2002)
Contact: Larry A. Cogburn
University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335
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ByIln.pk002.19 Normalized Chicken Reproductive Tract cDNA Library (pgrln.pk002.19 Normalized Chicken Reproductive Tract cDNA Library (pgrln) Gallus gallus cDNA clone pgrln.pk002.19 5' similar to gil450601 ref|NP_002724.1| protein kinase, AMP-activated, gamma 1 non-catalytic subunit; AMPK gamma 1; Protein kinase, AMP-activated, gamma 1, mRNA sequence.
                                                                                                                                                                               BM440762.1 GI:18471537
EST.
Chicken.
Gallus gallus
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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Tel: 302-831-1335
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Location/Qualifiers
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/lab_host="E. col1 EMDH10B"
/note="Vector: pCMVSPOR76; Library made from equivalent pools of total RNA isolated from each tissue (embryonic muscle 33.3%; juvenile muscle 33.3%; and epiphyseal growth plate 33.3% of the final RNA pool). Single pass sequencing from 5'-end"
139 c 137 g 133 t
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/clone_lib="Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate cDNA library (pgm2n)"
/sex="Male and Female"
                                                                                                                                                                      1 to 647)
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/db_xref="taxon:9031"
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/strain-"Commercial broiler and
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BASE COUNT
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                                                                                                                                                                                         Cellular Immunology
Heinrich-Pette-Institute
Martinistr. 52, 20251 Hamburg, Germany
Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                        Abdrakhmanov,I., Lödygin,D., Geroth,P., Arakawa,H., Law,A., Plachy,J., Korn,B. and Buerstedde,J.M.
A large database of chicken bursal ESTs as a resource for the analysis of vertebrate gene function Genome Res. 10 (12), 2062-2069 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (bases 1 to 649)
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AJ395115 dkfz426 Gallu:
AJ395115
AJ395115.1 GI:7125706
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                                                                                                 /organism="Gallus gallus"
/strain="CB"
/db_xref="taxon:9031"
/clone="9102r1"
/clone_lib="dkfz426"
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Location/Qualifiers
                                                                /tissue_type="Bursa of Fabricius"
227 c 155 g 137 t
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/note="Vector: pCMVSPORT6; Library made from three RNA pools from each tissue (testis 25%, ovary 25%, oviduct 50% of final RNA pool); Single pass sequence from 5'-end"
222 c 160 g 128 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="Testis, ovary and oviduct"
/dev_stage="Various stages;embryonic, po
and sexually-mature"
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/sex-"Male and Female"
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/strain="Commercial broil
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                                                                                            yr70c12.r1 Soares fetal liver sg
IMAGE:210646 5', mRNA sequence.
H64260
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                  EST
                                  Homo sapiens
                                                                              H64260.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Abdrakhmanov,I., Lodygin,D., Geroth,P., Arakawa,H., Law,A., Plachy,J., Korn,B. and Buerstedde,J.M.
A large database of chicken bursal ESTs as a resource for the analysis of vertebrate gene function Genome Res. 10 (12), 2062-2069 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Archosauria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathāe; Galliformes; Phasianidae; Phasianidae; Cases 1 to 758)
                                                  human
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AJ396118 dkfz426 Gallus
AJ396118
AJ396118.1 GI:7127728
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Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.
Location/Qualifiers
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Cellular Immunology
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                                                                              GI:1023000
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238 c 186 g 166 t
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                                                                   62 atccaagatttgggcatcggcacattccgagacttggc 99
                                                                                       CTGGATGAGCTTGGAATAGGAACGTACCACAACATTGC
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4444 Forest Park Parkway, Box 8501, St. Louis, MO
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 933
High quality sequence stops: 383
Source: IMAGE Consortium, LLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 413)
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Gish, W., Hawkins Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins , M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, M., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., B., Wilson, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Geneme Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Source: IMAGE Consortium, LLNL
This clone is available royaltly free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Insert Length: 933 Std Error: 0.00
Seq primer: M13RP1
                                                                                                                                                                  Similarity
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Location/Qualifiers
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57.1%;
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
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US-07-866-979-3
US-08-466-9068-3
US-08-706-281A-3
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US-08-436-265-1
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1435 base pairs

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u.	ASSOCIATED PROTEIN uticals, Inc. uticals and the second se	> 1081165	3-739B-1 5-8404-1 6-845-1 2-714-1 1-416-1 9-958-1
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 Query Match
Best Local Similarity
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                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                           MMEDIA: PENAL LIBRARY: PENAL NE: 1452972
                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN TITLE OF INVENTION: KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lal, Preeti
APPLICANT: Goli, Surya K.
APPLICANT: Shah, Purvi
                                                                                               MMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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                                                                                                            STRANDEDNESS:
TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Billings, Lucy J
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                    LENGTH:
                                                                                                                                                                                                         TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 3174 POR CITY: Palo Alto
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                                                                                  PENITUT01
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ilarity 57.1%;
Conservative
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  30.5%;
57.1%;
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Score 30.8; DB 4; Pred. No. 0.11;
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        Length 1435;
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                                                                   Query Match 25... Best Local Similarity 58.6 Matches 51; Conservative
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                FEATURE:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: NO. 5532347nan, Kevin
REGISTRATION NUMBER: 35,303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC.DOS/MS.DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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CITY: Illinois
                     363 CTCATTGACGTGCTCATCTGTGGCTCCATGGTGTCCAGTCTCTGCTTCCTGGGCATCATT 422
                                                                                                                                                                                                                                                         FEATURE:
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TELEPHONE: 312-715-1000
TELEPAX: 312-715-1234
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62 atccaagatttgggcatcggcacattc 88
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                                   NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 19920
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10 South Wacker Drive, Suite
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                                                                       Score 29.4; DB Pred. No. 0.33; 0; Mismatches
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RESULT 5
US-08-706-281A-3
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Best Local Similarity
                                                                                                                                                                                                      Matches
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,906B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 30
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5849871nan, Kevin E
RECISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,154-H
TELECHMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
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                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cone, Roger D
APPLICANT: Mountjoy, Kathleen G
TITLE OF INVENTION: Melanocyte Stimulating Hormone Receptor
TITLE OF INVENTION: and Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
MCDonnell Boebnen Hulbert & Berghoff
ADDRESSEE: McDonnell Boebnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: cDNA to mRNA
                                                                                    423 GCTATAGACCGCTACATCTCCATCTTC 449
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LOCATION:
                                                                                                            62 atccaagatttgggcatcggcacattc 88
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Pred. No. 0.33;
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RESULT 6
US-09-201-746-3
; Sequence 3, Application US/09201746
; Patent No. 6268221
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Best Local Similarity
Matches 51; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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MEDICH TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/706,281A
FILING DATE: 04-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 6100048nan, Kevin
REGISTRATION NUMBER: 35,303
                                                                                                                                                                                                                                                                                                                             FEATURE
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ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                           363 CTCATTGACGTGCTCATCTGTGGCTCCATGGTGTCCAGTCTCTGCTTCCTGGGCATCATT 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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APPLICANT:
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                                                                                       423 GCTATAGACCGCTACATCTCCATCTTC 449
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                                                                                                        62 atccaagatttgggcatcggcacattc 88
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CITY: Chicago
STATE: IL
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TELEFAX: 312-913-0002
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Pred. No. 0.33;
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GENERAL INFORMATION:

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RESULI
US-09-097-231-3
: Sequence 3, Application US/09097231
: Patent No. 6278038
: GENERAL INFORMATION:
: APPLICANT: Cone, Roger D
: Chen, Wenbiao
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LOCATION:
US-09-201-746-3
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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APPLICANT: Mountjoy, Kathleen
TITLE OF INVENTION: Melanocyt
TITLE OF INVENTION: and Uses
NUMBER OF SEQUENCES: 8
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                  423 GCTATAGACCGCTACATCTCCATCTTC 449
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TYPE: nucleic acid
STRANDEDNESS: single
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                                      Low, Malcolm J
TITLE OF INVENTION: Mammalian Melanocortin Receptor and Uses
NUMBER OF SEQUENCES: 22
                    CORRESPONDENCE ADDRESS:
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E: IL
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ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
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960..1260
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Pred. No. 0.33;
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NAME/KEY: 3'UTR
LOCATION: 960..1260
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-097-231-3
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Best Local
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                                                         APPLICANT: Chen, Howard Y.
APPLICANT: Trumbauer, Myrna E.
TITLE OF INVENTION: BRADYKININ B2 RECEPTOR MODIFIED
TITLE OF INVENTION: NON-HUMAN ANIMALS
NUMBER OF SEQUENCES: 12
                       CORRESPONDENCE ADDRESS:
ADDRESSEE: John W. Wallen III
STREET: 126 E. Lincoln Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1260 base pairs
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                                                                                                                                                                                      APPLICANT:
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nes 51; Conserv
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NAME: NO. 6278038nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 96,886-C
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APPLICATION NUMBER: US/09/097,231
FILING DATE: 12-Jun-1998
CLASSIFICATION: CUNKNOWN>
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STRANDEDNESS: single
New Jersey
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                                                                                                                                Hess, John W.
Chen, Howard Y.
                                                                                                                                                                    Strader,
                                                                                                                                                                   Borkowski, Joseph A. Strader, Catherine D.
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58.6%;
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COUNTRY: ZIP: 070

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GENERAL INFORMATION:
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Best Local Similarity
Matches 41; Conserv
                                                                                                                                                                                                                                               ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-OOS
OPERATING PROPERSION OF THE PRO
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
PILING DATE: 27-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Wallen III, John W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Chen, Howard Y.
APPLICANT: Trumbanor Trumbano
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                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: BRADYKININ B2 RECEPTOR MODIFIED TITLE OF INVENTION: NON-HUMAN ANIMALS NUMBER OF SEQUENCES: 12
PRIOR APPLICATION DATA:
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LENGTH: 1378 base pairs
TYPE: nucleic acid
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 19234
TELECOMMUNICATION INFORMATION:
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STATE: N
COUNTRY:
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                                                       CLASSIFICATION:
                                                                                                                     FILING DATE:
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                                                                                                                                                      APPLICATION NUMBER:
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: New Jersey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Borkowski, Joseph A. Strader, Catherine D.
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65.1%;
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Pred. No. 1.
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RESULT 10
US-08-938-291A-3/c
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; MOLECULE TYPE: DNA (genomic)
PCT-US95-09383-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/08938291A Patent No. 6117673
                                                                              APPLICATION UNMER: US/08/938,29.
FILING DATE: September 26, 1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMER: 60/027,337
APPLICATION UNMER: 60/027,337
FILING DATE: October 11, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 228/172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 65.1 Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (908) 594-4720 INFORMATION FOR SEQ ID NO: 3
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                 SOFTWARE: FastSeq
CURRENT APPLICATION DATA:
                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lev, Sima
APPLICANT: Plowman, Gregory D.
APPLICANT: Schlessinger, Josep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1378 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wallen III, John W
                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      876 GCA 878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                816 CATGCTCCTGAATGTCGTGGGCTTCCTGCTGCCCCTGAGTGTCATCACCTTCTGCACGAT 875
                               TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A. ZIP: 90071-2066
                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
                                               TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 cca 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION:
                 67-3510
                               (213) 489-16
(213) 955-0440
                                                                                                                                                                                                                                                                                                   IBM Compatible
                                                                                                                                                                                                                 UMBER: US/08/938,291A
September 26, 1997
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65.1%;
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Pred. No. 1.2;
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COCATION: 79...5700

COTHER INFORMATION: \product=

OTHER INFORMATION: \channel*

US-08-336-257A-3
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Query Match 20.1
Best Local Similarity 55.4
Matches 51; Conservative
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Patent No. 5726035
GENERAL INFORMATION:
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                                                                                                                                                                                                                              TELEPHONE: (619) 238-0999
TELEFAX: (619) 238-0062
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5975 base pairs
                                                                                                                                                                         TOPOLOGY: no
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                           NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 54
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Harpoid, Michael M.
APPLICANT: Campbell, Kevin P.
TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS: ADDRESSE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
71P: 92101-2926
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STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               666 CACCTTGCAGAGCTTGTATGCGCACATGATGGGGAAGACCTGCTTCTTGTACTCCTCGAT 607
                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM COR
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/0 FILING DATE: 07-NOV-1994
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nes 54; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 caagitccigcacatciitggitcccigcigccccggccciccitcctctaccgcactai 63
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                                                                                                                                                                        not relevant
E: Genomic DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Steven B.
                   26.18;
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   Score 26.4; D
Pred. No. 6.2;
0; Mismatches
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                                                                                                        "Alpha-1 subunit of animal calcium
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                                 DB 1;
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   41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44;
                               Length 5975;
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   Indels
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   0;
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   Gaps
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                                                                                                             Matches
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                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: ULMER, DUANE C
REGISTRATION NUMBER: 34,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC COM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1734
                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: DUANE C ULMER
 837
                                                897 CTGAGATCCCTAGACAGATTTATTTCCCAACTTCTCTCAGCCGGCTCCCTCAGGGCAAAT 838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: A NOVEL FAMILY OF HIGH AFFINITY,
TITLE OF INVENTION: MODIFIED ANTIBODIES FOR CANCER TREATMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: MIDLAND
STATE: MICHIGAN
COUNTRY: USA
ZIP: 48641-1967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
              62 atccaagatttg 73
                                                                                                                         Local Similarity
                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE:
                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                      ENGTH:
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                                                                                                             43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION:
                                                                                                                                                                                                                       nucleic acid
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                                                                                                                                                                                                                                     1984 base pairs
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                                                                                                             Conservative
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RIXON, MARK W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KAPLAN, DONALD A SCHOLOM, JEFFREY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANDERSON,
                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                                                               (517)
                                                                                                                                                                                                            double
                                                                                                                       25.3%;
59.7%;
                                                                                                                                                                                                                                                                            636-8104
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                                                                                                                                                                                                                                                                                                                   34,941
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                                                                                                                                                                                                                                                                                                           C-37
                                                                                                                       Score 25.6;
Pred. No. 7.
                                                                                                         ed. No. 7.9;
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Version #1.25
                                                                                                                                   DB 2;
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                                                                                                                                   Length 1984;
                                                                                                          Indels
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                                                                                                                                                                                                                                              RESULT 14
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                                                                                                                                                              Sequence 1, Application US/08481337A Patent No. 5863738 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/479, 285
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/040687
FILING DATE: 31-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: ULMER, DUANE C
REGISTRATION NUMBER: 34,941
REFERENCE/DOCKET NUMBER: C-37,075C
TELECOMMUNICATION INFORMATION:
                                          APPLICANT: TEN DIJKE, Peter
APPLICANT: HELDIN, Carl-Henrik
APPLICANT: MIYAZONO, Kohei
APPLICANT: SAMPATH, Kuber T.
TITLE OF INVENTION: Morphogenic Protein-Specific Cell
TITLE OF INVENTION: Surface Receptors and Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (517) 636-8104 INFORMATION FOR SEQ ID NO: 16
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                   CORRESPONDENCE ADDRESS
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                                     NUMBER OF SEQUENCES:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SONTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: A NOVEL FAMILY OF HIGH AFFINITY,
TITLE OF INVENTION: MODIFIED ANTIBODIES FOR CANCER TREATMENT
NUMBER OF SEQUENCES: 74
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: DUANE C ULMER
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                                                                                                                                                                                                                                                                                                                    62 atccaagatttg 73
   ADDRESSEE:
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RIXON, MARK W
ANDERSON, WH KERI
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Testa, Hurwitz & Thibeault
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Pred. No. 7.9;
0; Mismatches
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US-08-696-268B-1/c
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Best Local Similarity
Matches 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08696268B Patent No. 5968752
                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PLAN PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/696,268B
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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[NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1509 base pairs
                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hu
STREET: 125 High St.
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                 APPLICANT: ICHIJO, HIDENORI
APPLICANT: NISHITOH, HIDEKI
APPLICANT: SAMPATH, KUBER T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MEYERS, Thomas C.
REGISTRATION NUMBER: 36,9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: cDNA
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                     STREET: 125 |
CITY: Boston
                                                                                                                                                             COUNTRY: USA
ZIP: 02110
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LOCATION: 1..1509
OTHER INFORMATION:
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CITY: B
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TOPOLOGY: linear
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FILING DATE: 02-JUN-1995
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                                                US/08/696,268B
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                                                                              Version
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